

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:41:26 ; Search time 70.0319 Seconds  
(without alignments)  
1530.851 Million cell updates/sec

Title: US-10-088-703A-2

Perfect score: 1238  
Sequence: 1 MDTESRRANLALPQPPSSV.....YSATYSELDGEMSPIDL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	244	2 AAW75918	Human bet
2	1238	100.0	244	4 AAB72900	Human IGE
3	1238	100.0	244	4 AAB74447	Human wil
4	1238	100.0	244	5 ABP65043	Human mem
5	1238	100.0	244	5 AAU88021	Human IGE
6	1238	100.0	244	8 ADQ90468	Human IGE
7	1231	99.4	244	2 AAW29149	Human hig
8	910	73.5	195	4 AAB74448	Human var
9	697.5	56.3	235	5 ABP65047	Mouse mem
10	697.5	56.3	235	5 AAU88020	Mouse IGE
11	697.5	56.3	235	8 ADQ90467	Mouse IGE
12	645.5	52.1	243	2 AAR42341	Subunit o
13	645.5	52.1	243	5 ABP65048	Rat membr
14	645.5	52.1	246	2 AAR14770	Beta subu
15	645.5	52.1	246	2 AAR42337	Human Pce
16	636.5	51.4	243	2 AAR05026	Beta subu
17	283	22.9	112	2 AAR05027	Deleted f
18	283	22.9	115	2 AAR14771	Truncated
19	210	17.0	244	4 AAG63825	Immunoglo
20	209	16.9	244	5 ABP65036	Mouse mem
21	201.5	16.3	247	5 ABP65038	Mouse mem
22	200.5	16.2	247	4 AAE05353	Mouse hig
23	200.5	16.2	247	5 ABB72363	Murine pr
24	196	15.8	268	5 ABP65040	Mouse mem

25	191	15.4	197	7	ADN39134	Cancer/an
26	190	15.3	220	5	ABP60317	Human pol
27	190	15.3	220	5	ABP65023	Human mem
28	190	15.3	220	6	ABP55608	Amino aci
29	190	15.3	220	7	ADN39992	Cancer/an
30	190	15.3	220	8	ADP25105	PRO polyp
31	190	15.3	220	8	ADU06669	Novel bro
32	190	15.3	239	2	AAW96745	High affi
33	190	15.3	239	3	AAW50174	Human hig
34	190	15.3	239	7	ADK65835	Angiogene
35	190	15.3	245	3	AAW94973	Human sec
36	190	15.3	246	5	ADR41417	Human CD-
37	189.5	15.3	267	2	AAW15224	Human rec
38	189.5	15.3	267	6	ADA10964	Human cdn
39	189.5	15.3	273	4	ABG17004	Novel hum
40	189.5	15.3	299	3	AAW91352	Human sec
41	189.5	15.3	308	5	ADR41397	Human CD-
42	188	15.2	231	5	ADR41416	Human CD-
43	186.5	15.1	214	6	ADA83822	Human MS4
44	186	15.0	267	5	ABP65045	Human mem
45	186	15.0	267	7	ADD13125	Human MS4

## ALIGNMENTS

RESULT 1  
AAW75918  
ID AAW75918 standard; protein; 244 AA.

XX AC AAW75918;

DT 13-NOV-1998 (first entry)

DE Human beta subunit of Fc epsilon RI polypeptide sequence.

XX KW Human beta subunit of Fc epsilon RI; ARAM; Fc epsilon RI beta chain;  
KW antigen recognition activation motif; human beta subunit; allergy;  
KW high-affinity immunoglobulin E receptor.

XX OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Domain	60..80
FT	Domain	/note= "transmembrane domain"
FT	Domain	99..118
FT	Domain	/note= "transmembrane domain"
FT	Domain	129..150
FT	Domain	/note= "transmembrane domain"
FT	Domain	181..201
FT	Domain	/note= "transmembrane domain"

US5807988-A.

PD 15-SEP-1998.

PF 24-FEB-1994; 94US-00201879.

PR 16-APR-1992; 92US-00869933.

PR 16-APR-1993; 93WO-US003419.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Jouvin M, Kinet J;

XX WPI; 1998-520207/44.

DR N-PSDB; AAW54661.

XX Human IgE receptor beta subunit protein - and corresponding peptide(s)  
and fusion protein.

PS Claim 2; Col 43-44; 55pp; English.

XX

CC This represents the polypeptide sequence of a human beta subunit of Fc  
 CC epsilon RI (high-affinity immunoglobulin E receptor). The invention  
 CC provides a peptide fragment (AAW75917) from the human Fc epsilon RI beta  
 CC subunit protein that contains the amino acid sequence of an ARAM (antigen  
 CC recognition activation motif). Aspects of the invention are methods and  
 CC compositions to inhibit the function of human beta subunit, thereby  
 CC treating or preventing allergic reactions  
 XX  
 SQ Sequence 244 AA;

Query Match 100.0%; Score 1238; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;  
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLWTLVKKEQEF 60  
 DB 1 MDTESRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLWTLVKKEQEF 60  
 QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFSSFKAGYPPFWGAIFFSISGMLSIISER 120  
 DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFSSFKAGYPPFWGAIFFSISGMLSIISER 120  
 QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETKCFMASFSTE 180  
 DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETKCFMASFSTE 180  
 QY 181 IVVWMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240  
 DB 181 IVVWMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240  
 QY 241 PIDL 244  
 DB 241 PIDL 244

RESULT 2  
 AAB72900  
 ID AAB72900 standard; protein; 244 AA.  
 XX  
 AC AAB72900;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Human IGERB SEQ ID NO: 3.  
 XX  
 KW Human; immunoglobulin E receptor beta chain; IGERB; chromosome 11q13;  
 KW allergy; asthma; rhinitis; eczema; single nucleotide polymorphism; SNP;  
 KW atopy; probe; PCR primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200114588-A1.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 11-AUG-2000; 2000WO-US022175.  
 XX  
 PR 24-AUG-1999; 99US-0150423P.  
 XX  
 XX (GENA-) GENAISANCE PHARM INC.  
 PA (NAND/) NANDABALAN K.  
 XX  
 PI Denton RR, Klieem SE, Stephens JC;  
 XX  
 XX WPI; 2001-226623/23.  
 DR N-PSDB; AAF92145.  
 XX  
 PT Novel polynucleotide useful for therapeutic purposes, comprises  
 PT nucleotide polymorphisms in immunoglobulin E receptor beta chain gene.  
 XX  
 XX Claim 10; Page '59-60; 89pp; English.  
 PS  
 CC The present invention provides the protein and coding sequences of

CC several polymorphic variants of the human immunoglobulin E receptor beta  
 CC chain (IGERB). These contain single nucleotide polymorphisms (SNPs) which  
 CC may be indicative of a predisposition to atopy, allergy, asthma, rhinitis  
 CC and eczema. Also provided are the sequences of probes and primers for use  
 CC in identifying the genotype of an individual with regards to the IGERB  
 CC gene. The IGERB gene is found at human chromosome 11q13. The sequences  
 CC are all useful in therapeutics. The present sequence is the IGERB protein  
 XX  
 SQ Sequence 244 AA;

Query Match 100.0%; Score 1238; DB 4; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;  
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLWTLVKKEQEF 60  
 DB 1 MDTESRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLWTLVKKEQEF 60  
 QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFSSFKAGYPPFWGAIFFSISGMLSIISER 120  
 DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFSSFKAGYPPFWGAIFFSISGMLSIISER 120  
 QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETKCFMASFSTE 180  
 DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETKCFMASFSTE 180  
 QY 181 IVVWMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240  
 DB 181 IVVWMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240  
 QY 241 PIDL 244  
 DB 241 PIDL 244

RESULT 3  
 AAB74447  
 ID AAB74447 standard; protein; 244 AA.  
 XX  
 AC AAB74447;  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Human wild-type Fc epsilon RI beta chain.  
 XX  
 KW Human; Fc epsilon RI beta chain; immunoglobulin E; allergy; atopy;  
 KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200121816-A1.  
 XX  
 PD 29-MAR-2001.  
 XX  
 PF 21-SEP-2000; 2000WO-US025877.  
 XX  
 PR 21-SEP-1999; 99US-0154924P.  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 XX  
 PI Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;  
 XX  
 XX WPI; 2001-266077/27.  
 DR N-PSDB; AAF77688.  
 XX  
 PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)  
 PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by  
 PT contacting cell or administering to subject, a Fc epsilon beta chain variant.  
 XX  
 XX Disclosure; Page 48-49; 55pp; English.  
 XX  
 CC The present invention describes a method of inhibiting the expression of

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OM protein - protein search; using sw model

Run on: March 2, 2006, 18:45:16 ; Search time 27.2346 Seconds  
(without alignments)  
862.024 Million cell updates/sec

Title: US-10-088-703A-2  
Perfect score: 1238  
Sequence: 1 MDTESNRRANLALPQEPSSV.....YSATYSELEDPGEMSPIDL 244

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	244	2	IgE Fc receptor be
2	766	61.9	152	2	IgE receptor beta
3	697.5	56.3	235	2	IgE Fc receptor be
4	645.5	52.1	243	2	high-affinity IgE
5	185.5	15.0	214	2	IgE receptor beta
6	127	10.3	297	1	B-cell surface ant
7	123.5	10.0	200	2	testis expressed t
8	111	9.0	826	2	desmocollin, type
9	111	9.0	896	2	desmocollin, type
10	103.5	8.4	291	2	B-cell surface ant
11	96.5	7.8	921	2	conserved hypotet
12	94	7.6	466	2	amino acid antipor
13	90	7.3	629	2	hypothetical prote
14	89	7.2	904	1	nitrate reductase
15	86.5	7.0	701	2	Na+/H+ antiporter
16	86	6.9	722	2	hypothetical prote
17	85.5	6.9	377	2	conserved hypotet
18	85	6.9	492	2	NADH2 dehydrogenas
19	84.5	6.8	207	2	alkaline phosphata
20	84.5	6.8	318	2	probable integral
21	84.5	6.8	659	2	hypothetical prote
22	84	6.8	681	2	glvr-1 protein - m
23	83.5	6.7	380	2	NADH dehydrogenase
24	83.5	6.7	470	2	hypothetical prote
25	83.5	6.7	473	2	probable membrane
26	83.5	6.7	669	2	hypothetical prote
27	83.5	6.7	4447	2	polyketide synthas
28	83	6.7	253	2	hypothetical prote
29	83	6.7	440	2	branched-chain ami

## ALIGNMENTS

## RESULT 1

A42806  
IgE Fc receptor beta chain - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 09-Jul-2004  
C:Accession: A42806; S21154  
R:Kuester, H.; Zhang, L.; Brini, A.T.; MacGlashan, D.W.J.; Kinet, J.P.  
J. Biol. Chem. 267, 12782-12787, 1992  
A:Title: The gene and cDNA for the human high affinity immunoglobulin E receptor beta  
A:Reference number: A42806; MUID:92316966; PMID:1535625  
A:Accession: A42806  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-244 <KUE>  
A:Cross-references: UNIPROT:Q01362; UNIPARC:UPI0000038E6F; GB:M89796; NID:G337417; PII  
R:Maekawa, K.; Inagawa, N.; Tanaka, Y.; Harada, S.  
FEBS Lett. 302, 161-165, 1992  
A:Title: Determination of the sequence coding for the beta subunit of the human high-  
A:Reference number: S21154; MUID:92339505; PMID:1386024  
A:Accession: S21154  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-244 <MAE>  
A:Cross-references: UNIPARC:UPI0000038E6F; GB:D10583; NID:G219881; PIDN:BAA01440.1; P:  
C:Genetics:  
A:Introns: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3  
C:Keywords: immunoglobulin receptor; transmembrane protein

Query Match	100.0%;	Score	1238;	DB 2;	Length	244;
Best Local Similarity	100.0%;	Pred. No.	3.7e-107;			
Matches	244;	Conservative	0;	Mismatches	0;	Gaps
QY	1	MDTESNRRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKKSASPPHLTWTVLVKKQEF	60			
DB	1	MDTESNRRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKKSASPPHLTWTVLVKKQEF	60			
QY	61	LGVTQTLTAMICLCFGTVCSVLDSHIEDGFSSPKAGYFPFWGALFFESISGMLSIISER	120			
DB	61	LGVTQTLTAMICLCFGTVCSVLDSHIEDGFSSPKAGYFPFWGALFFESISGMLSIISER	120			
QY	121	RNATVIVRSLGANTASSIAGGTGITILLINLKSLAYTHIHSCQKFFETKCFMAGFSPE	180			
DB	121	RNATVIVRSLGANTASSIAGGTGITILLINLKSLAYTHIHSCQKFFETKCFMAGFSPE	180			
QY	181	IIVVMMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPGEMSP	240			
DB	181	IIVVMMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPGEMSP	240			
QY	241	PIDL 244				
DB	241	PIDL 244				

hypothetical prote  
probable NreB prot  
hypothetical prote  
amino acid permeas  
probable permease  
amino acid transpo  
nitrate reductase  
hypothetical prote  
multidrug resistan  
NADH2 dehydrogenas  
hydroxymethylgluta  
ferric vibriobacti  
hypothetical prote  
calcium/proton ant.  
presenilin-beta -

JH0751

### RESULT 3

[illegible]

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: March 2, 2006, 18:44:51 ; Search time 180.082 Seconds  
 (without alignments)  
 955.947 Million cell updates/sec.  
 Title: US-10-088-703A-2  
 Perfect score: 1238  
 Sequence: 1 MDTESNRRANLALPQEPSSV.....YSATYSELDPGEMSPPIDL 244

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 2166443 seqs, 705528306 residues  
 Total number of hits satisfying chosen parameters: 2166443  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
 Database : Uniprot 05.80:.\*  
 1: uniprot\_sprot.\*  
 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	244	1 FCERB_HUMAN	Q01362 homo sapien
2	1238	100.0	244	2 Q54A81_HUMAN	Q54A81 homo sapien
3	766	61.9	152	2 Q14298_HUMAN	Q14298 homo sapien
4	697.5	56.3	235	1 FCERB_MOUSE	P20490 mus musculus
5	660.5	53.4	243	2 Q8WJ38_PIG	Q8WJ38 sus scrofa
6	645.5	52.1	243	1 FCERB_RAT	P13386 rattus norv
7	209	16.9	244	1 M4A6B_MOUSE	Q99N09 mus musculus
8	205	16.6	247	2 Q5X1J0_RAT	Q5X1J0 rattus norv
9	201.5	16.3	247	1 M4A6D_MOUSE	Q99N07 mus musculus
10	186	15.8	287	1 M4A8A_MOUSE	Q99N10 mus musculus
11	190	15.3	239	1 M4A4A_HUMAN	Q96J95 homo sapien
12	189.5	15.3	267	1 M4A12_HUMAN	Q99XJ0 homo sapien
13	186.5	15.1	214	1 MS4A3_HUMAN	Q96J15 homo sapien
14	185.5	15.0	213	1 MS4A3_MOUSE	Q920c4 mus musculus
15	185.5	15.0	213	2 Q810H7_MOUSE	Q810h7 mus musculus
16	185.5	15.0	213	2 Q532U3_MOUSE	Q532u3 mus musculus
17	183	14.8	220	2 Q4JF27_HUMAN	Q4Jf27 homo sapien
18	182	14.7	679	2 Q96J4A_HUMAN	Q96J4a homo sapien
19	176.5	14.3	217	1 M4A6C_MOUSE	Q99N08 mus musculus
20	174	14.1	250	1 M4A8B_HUMAN	Q9B1y9 homo sapien
21	166	13.4	222	2 Q58DM5_BOVIN	Q58dm5 bos taurus
22	165	13.3	240	1 MS4A7_HUMAN	Q99Ww8 homo sapien
23	165	13.3	240	2 Q6TAG8_HUMAN	Q6tag8 homo sapien
24	161.5	13.0	241	2 Q567K1_BRARE	Q567k1 brachydanio
25	161	13.0	55	2 Q924W0_MUSSP	Q924w0 mus spretus
26	161	13.0	55	2 P97890_MUSMM	P97890 mus musculus
27	161	13.0	234	2 Q99N04_MOUSE	Q99N04 mus musculus
28	158	12.8	267	2 Q8BV59_MOUSE	Q8bv59 mus musculus
29	157	12.7	234	2 Q8R3W1_MOUSE	Q8r3w1 mus musculus
30	154.5	12.5	197	2 Q810P8_MOUSE	Q810p8 mus musculus
31	152	12.3	248	1 M4A6A_HUMAN	Q9h3w1 homo sapien

RESULT 1  
 FCERB\_HUMAN  
 ID FCERB\_HUMAN STANDARD; PRT; 244 AA.  
 AC Q01362;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE High affinity immunoglobulin epsilon receptor beta-subunit (FCERI)  
 DE (I98 FC receptor, beta-subunit) (Fc epsilon receptor I beta-chain).  
 GN Name=MS4A2; Synonyms=FCER1B, IGER;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92316966; PubMed=1535625;  
 RA Kuester H., Zhang L., Brini A.T., Macglashan D.W., Kinet J.-P.;  
 RT "The gene and cDNA for the human high affinity immunoglobulin E  
 receptor beta chain and expression of the complete human receptor.";  
 RL J. Biol. Chem. 267:12782-12787(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92339505; PubMed=1386024; DOI=10.1016/0014-5793(92)80430-O;  
 RA Maekawa K., Inagawa N., Tanaka Y., Harada S.;  
 RT "Determination of the sequence coding for the beta subunit of the  
 human high-affinity IGE receptor.";  
 RL FEBS Lett. 302:161-165(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Lung;  
 RX MEDLINE=22388957; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]

Q8b129 mus musculus  
 Q5rlm8 felis silve  
 Q9d3f6 mus musculus  
 Q80wf0 rattus norv  
 Q5blb6 brachydanio  
 Q567h8 brachydanio  
 Q99n05 mus musculus  
 Q4tai3 tetraodon n  
 Q8n5u1 homo sapien  
 P11836 homo sapien  
 Q5m796 xenopus tro  
 Q661d5 brachydanio  
 Q9es61 mus musculus  
 Q9h3v2 homo sapien

RP VARIANT GLY-237.  
RX MEDLINE=96414302; PubMed=8817330; DOI=10.1093/hmg/5.7.959;  
RA Hill M.R., Cooke W.O.;  
RT "A new variant of the beta subunit of the high-affinity receptor for  
RT immunoglobulin E (Fc epsilon RI-beta E237G): associations with  
RT measures of atopy and bronchial hyper-responsiveness.";  
RL Hum. Mol. Genet. 5:959-962(1996).  
RN [5]  
RP VARIANT GLY-237.  
RX MEDLINE=96440420; PubMed=8842731; DOI=10.1093/hmg/5.8.1129;  
RA Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,  
RA Hopkin J.;  
RT "Association between atopic asthma and a coding variant of Fc-epsilon-  
RT RI-beta in a Japanese population.";  
RL Hum. Mol. Genet. 5:1129-1130(1996).  
RN [6]  
RP ERRATUM.  
RX MEDLINE=97123518; PubMed=8968765;  
RA Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,  
RA Hopkin J.;  
RL Hum. Mol. Genet. 5:2068-2068(1996).  
CC -1- FUNCTION: Binds to the Fc region of immunoglobulins epsilon. High  
CC affinity receptor. Responsible for initiating the allergic  
CC response. Binding of allergen to receptor-bound IgE leads to cell  
CC activation and the release of mediators (such as histamine)  
CC responsible for the manifestations of allergy. The same receptor  
CC also induces the secretion of important lymphokines.  
CC -1- SUBUNIT: Tetramer of an alpha chain, a beta chain, and two  
CC disulfide linked gamma chains.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Found on the surface of mast cells and  
CC basophils.  
CC -1- POLYMORPHISM: Variant Glu-237 has been found to be present in  
CC about 5.3% of a 1004 individuals population sample in Australia.  
CC It seems to be a risk factor for atopic dermatitis and asthma.  
CC -1- SIMILARITY: Belongs to the MS4A family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC ENBL; D10583; BAA01440.1; -; mRNA.  
CC DR ENBL; M89796; AAA60269.1; -; Genomic DNA.  
CC DR ENBL; BC074800; AAH74800.1; -; mRNA.  
CC DR ENBL; BC074843; AAH74843.1; -; mRNA.  
CC DR PIR; A42806; A42806.  
CC DR Ensembl; ENSG00000149534; Homo sapiens.  
CC DR HGNC; HGNC:7316; MS4A2.  
CC DR MTM; 147138; -.  
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC DR GO; GO:0005262; C:calcium channel activity; TAS.  
CC DR GO; GO:008283; P:cell proliferation; TAS.  
CC DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
CC DR GO; GO:0006959; P:numoral immune response; TAS.  
CC DR InterPro; IPR007237; CD20/IgFcrcept.  
CC DR Pfam; PF04103; CD20; 1.  
CC DR IGE-binding protein; Multigene family; Polymorphism; Receptor;  
CC Transmembrane. 1  
KW TOPO\_DOM 1 59 Cytoplasmic (Potential).  
FT TRANSMEM 60 79 Potential.  
FT TOPO\_DOM 80 97 Extracellular (Potential).  
FT TRANSMEM 98 117 Potential.  
FT TOPO\_DOM 118 130 Cytoplasmic (Potential).  
FT TRANSMEM 131 150 Potential.  
FT TOPO\_DOM 151 180 Extracellular (Potential).  
FT TRANSMEM 181 200 Potential.  
FT TOPO\_DOM 201 244 Cytoplasmic (Potential).  
FT VARIANT 237 237 E -> G (in dbSNP:569108).  
FT  
SQ SEQUENCE 244 AA; 26534 MW; CE523102D5F567AF CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.3e-105;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSPFKAGYPFWGAIFFSISGMLSIIISER 120  
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DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHIHSCQKFFETKCFMASFSTE 180  
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DB 241 PIDL 244  
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ID Q54A81 HUMAN PRELIMINARY; PRT; 244 AA.  
AC Q54A81;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Fc-epsilon receptor I beta-chain.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=12697656; DOI=10.1093/intimm/dxg055;  
RA Akizawa Y., Nishiyama C., Hasegawa M., Maeda K., Nakahata T.,  
RA Okumura K., Ra C., Ogawa H.;  
RA "Regulation of human FcepsilonRI beta chain gene expression by Oct-  
RT 1.";  
RT Int. Immunol. 15:549-556(2003).  
RL EMBL; AB080913; BAC66486.1; -; Genomic DNA.  
KW Receptor.  
SQ SEQUENCE 244 AA; 26533 MW; CE523102D5F567AF CRC64;  
Query Match 100.0%; Score 1238; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.3e-105;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MOTESNRRANLALPOEPSSVPAFAVELEISPOEVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60  
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DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSPFKAGYPFWGAIFFSISGMLSIIISER 120  
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHIHSCQKFFETKCFMASFSTE 180  
DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHIHSCQKFFETKCFMASFSTE 180  
QY 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240  
DB 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240  
QY 241 PIDL 244  
DB 241 PIDL 244

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:46:52 ; Search time 20.5649 seconds  
(without alignments)  
980.936 Million cell updates/sec

Title: US-10-088-703A-2

Perfect score: 1238  
Sequence: 1 MDTESNRANLALPQEPSSV.....YSATYSELDPGEMSPIDL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	244	1	US-07-869-933-32
2	1238	100.0	244	1	US-08-201-879A-3
3	1238	100.0	244	2	US-09-103-663-32
4	1238	100.0	244	2	US-09-949-016-5892
5	1238	100.0	244	2	US-09-949-016-8329
6	697.5	56.3	235	1	US-07-869-933-34
7	697.5	56.3	235	1	US-08-201-879A-5
8	697.5	56.3	235	2	US-09-103-663-34
9	645.5	52.1	243	1	US-07-869-933-29
10	645.5	52.1	243	1	US-07-869-933-33
11	645.5	52.1	243	1	US-08-201-879A-4
12	645.5	52.1	243	1	US-08-916-902A-4
13	645.5	52.1	243	1	US-09-213-389-4
14	645.5	52.1	243	2	US-09-103-663-29
15	645.5	52.1	243	2	US-09-103-663-33
16	645.5	52.1	246	1	US-07-869-933-23
17	645.5	52.1	246	2	US-09-103-663-23
18	200.5	16.2	247	2	US-09-124-864-49
19	190	15.3	239	1	US-08-916-902A-1
20	190	15.3	239	1	US-09-213-389-1
21	190	15.3	239	2	US-10-164-595-74
22	189.5	15.3	239	2	US-09-904-615-73
23	189.5	15.3	239	2	US-10-054-988-73
24	185.5	15.0	214	1	US-08-318-492-4
25	185.5	15.0	214	1	US-08-707-340-4
26	185.5	15.0	214	1	US-08-916-902A-3
27	185.5	15.0	214	1	US-08-994-578-4

28	185.5	15.0	214	1	US-09-213-389-3	Sequence 3, Appli
29	183.5	14.8	307	2	US-09-904-615-142	Sequence 142, App
30	183.5	14.8	307	2	US-10-054-988-142	Sequence 142, App
31	174	14.1	250	2	US-09-702-705-1677	Sequence 1677, Ap
32	174	14.1	250	2	US-09-736-457-1677	Sequence 1677, Ap
33	174	14.1	250	2	US-09-671-325-1677	Sequence 1677, Ap
34	174	14.1	250	2	US-09-658-824-1677	Sequence 1677, Ap
35	174	14.1	250	2	US-10-017-754-1677	Sequence 1677, Ap
36	174	14.1	250	2	US-10-017-754-2004	Sequence 2004, Ap
37	174	14.1	250	2	US-09-651-563-1677	Sequence 1677, Ap
38	166	13.4	250	2	US-10-017-754-1874	Sequence 1874, Ap
39	166	13.4	286	2	US-10-017-754-1878	Sequence 1878, Ap
40	166	13.4	384	2	US-10-017-754-1876	Sequence 1876, Ap
41	152	12.3	248	2	US-09-489-847-207	Sequence 207, App
42	152	12.3	273	2	US-09-489-847-363	Sequence 363, App
43	144	11.6	204	2	US-09-904-615-117	Sequence 117, App
44	144	11.6	204	2	US-10-054-988-117	Sequence 117, App
45	142.5	11.5	225	2	US-09-855-323-14	Sequence 14, Appli

## ALIGNMENTS

RESULT 1  
US-07-869-933-32  
; Sequence 32, Application US/07869933  
; Patent No. 5770396  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/869,933  
; FILING DATE: 19920416  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO.: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; STRAIN: FcR1 beta subunit  
; US-07-869-933-32

Query Match 100.0%; Score 1238; DB 1; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.2e-132;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTWLTVLKKEQEF 60  
QY 61 LGVTQILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
Db 61 LGVTQILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
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Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180  
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Db 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240  
QY 241 PIDL 244  
Db 241 PIDL 244

## RESULT 2

US-08-201-879A-3  
; Sequence 3, Application US/08201879A  
; Patent No. 5807988  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; APPLICANT: JOUVIN, Marie-Helene  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; TITLE OF INVENTION: IMMUNOGLOBULIN E  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/201,879A  
; FILING DATE: 24-FEB-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/869,933  
; FILING DATE: 16-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/03419  
; FILING DATE: 16-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 40399/234/NIHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-201-879A-3

Query Match 100.0%; Score 1238; DB 1; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.2e-132;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTWLTVLKKEQEF 60  
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Db 61 LGVTQILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
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Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180  
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Db 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240  
QY 241 PIDL 244  
Db 241 PIDL 244

## RESULT 3

US-09-103-663-32  
; Sequence 32, Application US/09103663D  
; Patent No. 6171803  
; GENERAL INFORMATION:  
; APPLICANT: Kinet et al.  
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta  
; TITLE OF INVENTION: subunit of the high affinity receptor for  
; TITLE OF INVENTION: immunoglobulin E.  
; FILE REFERENCE: 50490  
; CURRENT APPLICATION NUMBER: US/09/103,663D  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 07/869,933  
; EARLIER FILING DATE: 1992-04-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-103-663-32

Query Match 100.0%; Score 1238; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.2e-132;  
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTWLTVLKKEQEF 60  
Db 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTWLTVLKKEQEF 60  
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Db 61 LGVTQILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180  
Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180  
QY 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240  
Db 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240  
QY 241 PIDL 244  
Db 241 PIDL 244

## RESULT 4

US-09-949-016-5892  
; Sequence 5892, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 18:50:58 ; Search time 67.8087 Seconds  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	697.5	56.3	235	US-10-433-287-50	Sequence 50, Appl
5	645.5	52.1	243	US-10-433-287-52	Sequence 52, Appl
6	209	16.9	244	US-10-433-287-28	Sequence 28, Appl
7	201.5	16.3	247	US-10-433-287-32	Sequence 32, Appl
8	200.5	16.2	247	US-09-866-050A-687	Sequence 687, App
9	196	15.8	268	US-10-433-287-36	Sequence 36, Appl
10	191	15.4	197	US-10-295-027-452	Sequence 452, App
11	191	15.4	220	US-10-015-115-103	Sequence 103, App
12	191	15.4	239	US-10-015-115-101	Sequence 101, App
13	190	15.3	220	US-10-295-027-1310	Sequence 1310, App
14	190	15.3	220	US-10-433-287-2	Sequence 2, Appli
15	190	15.3	220	US-10-015-115-102	Sequence 102, App
16	190	15.3	239	US-10-717-665-74	Sequence 74, Appl
17	190	15.3	239	US-09-374-046A-152	Sequence 152, App
18	190	15.3	245	US-10-616-263-152	Sequence 152, App
19	189.5	15.3	267	US-09-981-353-82	Sequence 82, Appl
20	189.5	15.3	273	US-10-450-763-47363	Sequence 47363, A
21	189.5	15.3	299	US-09-739-254-73	Sequence 73, Appl
22	189.5	15.3	299	US-09-904-615-73	Sequence 73, Appl
23	189.5	15.3	299	US-10-054-988-73	Sequence 73, Appl
24	189.5	15.3	214	US-10-157-031-104	Sequence 104, App
25	186.5	15.1	214	US-10-433-287-46	Sequence 46, Appl
26	186	15.0	267	US-10-433-287-44	Sequence 44, Appl
27	185.5	15.0	214	US-10-433-287-44	Sequence 44, Appl

28	184	14.9	240	5	US-10-484-148-7	Sequence 7, Appli
29	183.5	14.8	307	3	US-09-739-254-142	Sequence 142, App
30	183.5	14.8	307	3	US-09-904-615-142	Sequence 142, App
31	183.5	14.8	307	4	US-10-054-988-142	Sequence 142, App
32	178	14.4	227	5	US-10-450-763-49595	Sequence 49595, A
33	176.5	14.3	217	4	US-10-433-287-30	Sequence 30, Appl
34	174	14.1	250	3	US-09-736-457-1677	Sequence 1677, Ap
35	174	14.1	250	3	US-09-902-941-1677	Sequence 1677, Ap
36	174	14.1	250	3	US-09-849-626-1677	Sequence 1677, Ap
37	174	14.1	250	4	US-10-017-754-1677	Sequence 1677, Ap
38	174	14.1	250	4	US-10-017-754-2004	Sequence 2004, Ap
39	174	14.1	250	4	US-10-156-136-21	Sequence 21, Appl
40	174	14.1	250	4	US-10-113-872-1677	Sequence 1677, Ap
41	174	14.1	250	4	US-10-113-872-2004	Sequence 2004, Ap
42	174	14.1	250	4	US-10-283-017-1677	Sequence 1677, Ap
43	174	14.1	250	4	US-10-283-017-2004	Sequence 2004, Ap
44	174	14.1	250	4	US-10-295-027-624	Sequence 624, App
45	174	14.1	250	4	US-10-264-237-2566	Sequence 2566, Ap

## ALIGNMENTS

### RESULT 1

US-10-369-214-124  
; Sequence 124, Application US/10369214  
; Publication No. US2003023037A1  
; GENERAL INFORMATION:  
; APPLICANT: Groot, Pieter C.  
; APPLICANT: Berghenhegouwen van, Bram J.  
; APPLICANT: Oosterhout van, Antoon J.M.  
; TITLE OF INVENTION: Genes involved in immune related responses observed  
; TITLE OF INVENTION: with asthma  
; FILE REFERENCE: P53837US00  
; CURRENT APPLICATION NUMBER: US/10/369,214  
; PRIOR FILING DATE: 2003-02-15  
; PRIOR APPLICATION NUMBER: EP 00202867.8  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: PCT/NL01/00610  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 124  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(244)  
; OTHER INFORMATION: /note="Ige receptor beta chain"  
US-10-369-214-124

Query Match	100.0%;	Score 1238;	DB 4;	Length 244;
Best Local Similarity	100.0%;	Pred. No. 1.9e-122;		
Matches 244;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDTESNRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKLSASSPPLHTWLTVLKKEQEF	60	
Db	1	MDTESNRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKLSASSPPLHTWLTVLKKEQEF	60	
QY	61	LGVTQTLTAMICLCFCGTVCVSLDISHIEDGIFSSFKAGYPPFWGAIFFSISGMLSIISER	120	
Db	61	LGVTQTLTAMICLCFCGTVCVSLDISHIEDGIFSSFKAGYPPFWGAIFFSISGMLSIISER	120	
QY	121	RNATYVIRGSLGANTASSIAGGTGITILLINKKSLAYIIHSCQKFFETKCFMASFSTE	180	
Db	121	RNATYVIRGSLGANTASSIAGGTGITILLINKKSLAYIIHSCQKFFETKCFMASFSTE	180	
QY	181	IIVVMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPGEMSP	240	
Db	181	IIVVMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPGEMSP	240	
QY	241	PIDL 244		

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Db      241 PIDL 244
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RESULT 2
US-10-433-287-42
; Sequence 42, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-433-287-42
Query Match      100.0%; Score 1238; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-122; Indels 0; Gaps 0;
Matches 244; Conservative 0; Mismatches 0;

QY      1 MDTESNRANLALPQEPSSVPAPEVLEISPOEVSSGRLLKSASSPPLHTWTLVKKEQEF 60
Db      1 MDTESNRANLALPQEPSSVPAPEVLEISPOEVSSGRLLKSASSPPLHTWTLVKKEQEF 60

QY      61 LGVTOILTAMICLCFCGTWCVSLDISHIEGDISSFKAGYFPGWGAIFPSISGMLSIISER 120
Db      61 LGVTOILTAMICLCFCGTWCVSLDISHIEGDISSFKAGYFPGWGAIFPSISGMLSIISER 120

QY      121 RNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHIHSCOKFFETKCFWAGSFSTE 180
Db      121 RNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHIHSCOKFFETKCFWAGSFSTE 180

QY      181 IVVMMLFLTILGSAVSLTICGAGEELKGNKVPEDRVYBELNIYSATYSELEDPCGEMSP 240
Db      181 IVVMMLFLTILGSAVSLTICGAGEELKGNKVPEDRVYBELNIYSATYSELEDPCGEMSP 240

QY      241 PIDL 244
Db      241 PIDL 244
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RESULT 3
US-10-369-214-123
; Sequence 123, Application US/10369214
; Publication No. US20030232037A1
; GENERAL INFORMATION:
; APPLICANT: Groot, Pieter C.
; APPLICANT: Bergenhegouwen van, Bram J.
; APPLICANT: Oosterhout van, Antoon J.M.
; TITLE OF INVENTION: Genes involved in immune related responses observed
; TITLE OF INVENTION: with asthma
; FILE REFERENCE: P53837US00
; CURRENT APPLICATION NUMBER: US/10/369,214
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: EP 00202867.8
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00610
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 123
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (1)..(235)
; OTHER INFORMATION: /note="Ige receptor beta chain"
US-10-369-214-123
Query Match      56.3%; Score 697.5; DB 4; Length 235;
Best Local Similarity 57.7%; Pred. No. 3.8e-65;
Matches 142; Conservative 33; Mismatches 56; Indels 15; Gaps 4;

QY      1 MDTESNRANLAL--POEPSSVPAPEVLEISPOEVSSGRLLKSASSPPLHTWTLVKKEQ 58
Db      1 MDTESNRADLALPNQESSAPDIELLEASP-----AKAAPPKQTWRTFLKKEL 50

QY      59 EFLGVTOILTAMICLCFCGTWCVSLDISHIEGDISSFKAGYFPGWGAIFPSISGMLSIIS 118
Db      51 EFLGATQILVGLICLCFCGTIVCSLVVSDFDEEVLLLYKLGYPFWGAVLFLVSGFLSIIS 110

QY      119 EERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHIHSCOKFFETK-CFWASF 177
Db      111 ERKNTLYLVRSGLGANIVSSIAAGTGIAMLILNTNMFAY--MNNCKNVTEDDGCFCVASF 168

QY      178 STEIVVMMLFLTILGSAVSLTICGAGEELKGNKVPEDRVYBELNIYSATYSELEDPCGE 237
Db      169 TTELVLMLFLTILAFCSAVLFTIYRIGQELSKVPPDDRLYBELNVYSPYIYSELEDKGE 228

QY      238 MSPPID 243
Db      229 TSSPVD 234
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RESULT 4
US-10-433-287-50
; Sequence 50, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 50
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-433-287-50
Query Match      56.3%; Score 697.5; DB 4; Length 235;
Best Local Similarity 57.7%; Pred. No. 3.8e-65;
Matches 142; Conservative 33; Mismatches 56; Indels 15; Gaps 4;

QY      1 MDTESNRANLAL--POEPSSVPAPEVLEISPOEVSSGRLLKSASSPPLHTWTLVKKEQ 58
Db      1 MDTESNRADLALPNQESSAPDIELLEASP-----AKAAPPKQTWRTFLKKEL 50

QY      59 EFLGVTOILTAMICLCFCGTWCVSLDISHIEGDISSFKAGYFPGWGAIFPSISGMLSIIS 118
Db      51 EFLGATQILVGLICLCFCGTIVCSLVVSDFDEEVLLLYKLGYPFWGAVLFLVSGFLSIIS 110

QY      119 EERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHIHSCOKFFETK-CFWASF 177
Db      111 ERKNTLYLVRSGLGANIVSSIAAGTGIAMLILNTNMFAY--MNNCKNVTEDDGCFCVASF 168

QY      178 STEIVVMMLFLTILGSAVSLTICGAGEELKGNKVPEDRVYBELNIYSATYSELEDPCGE 237
Db      169 TTELVLMLFLTILAFCSAVLFTIYRIGQELSKVPPDDRLYBELNVYSPYIYSELEDKGE 228

QY      238 MSPPID 243
Db      229 TSSPVD 234
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Title: US-10-088-703A-2

Perfect score: 1238

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	186	15.0	267	6	US-10-506-443A-38
2	147.5	11.9	298	7	US-11-138-949-9
3	143.5	11.6	297	7	US-11-138-949-6
4	128	10.3	248	5	US-09-378-360A-610
5	127	10.3	297	7	US-11-138-949-7
6	127	10.3	297	7	US-11-190-364-25
7	127	10.3	297	7	US-11-190-364-25
8	127	10.3	297	7	US-11-147-780-25
9	127	10.3	297	7	US-11-147-780-26
10	123.5	10.0	199	7	US-11-179-018-2
11	111	9.0	896	7	US-11-080-991-98
12	106	8.6	20	6	US-10-485-788A-598
13	103.5	8.4	291	7	US-11-138-949-8
14	100	8.1	138	7	US-11-179-018-6
15	99.5	8.0	149	7	US-11-179-018-8
16	90.5	7.3	391	6	US-10-793-626-1236
17	83.5	6.7	230	7	US-11-072-512-3554
18	81.5	6.6	437	7	US-11-087-099-6210
19	81.5	6.6	452	6	US-10-793-626-1834
20	80	6.5	478	7	US-11-072-512-2616
21	79.5	6.4	756	6	US-10-330-773-731
22	79.5	6.4	935	6	US-10-995-561-1012
23	79.5	6.4	935	6	US-10-995-561-1013
24	78	6.3	237	7	US-11-108-172-1062
25	78	6.3	243	7	US-11-108-172-1122

26	78	6.3	446	7	US-11-108-172-1121	Sequence 1121, Ap
27	77	6.2	394	6	US-10-821-234-1194	Sequence 1194, Ap
28	76.5	6.2	972	6	US-10-821-234-1597	Sequence 1597, Ap
29	76	6.1	608	7	US-11-167-856-12	Sequence 12, Appl
30	74	6.0	172	7	US-11-036-797-36	Sequence 36, Appl
31	74	6.0	461	7	US-11-072-512-3584	Sequence 3584, Ap
32	74	6.0	479	7	US-11-087-099-2079	Sequence 2079, Ap
33	73.5	5.9	359	7	US-11-087-177-29	Sequence 29, Appl
34	73	5.9	344	7	US-11-108-172-1085	Sequence 1085, Ap
35	72.5	5.9	268	6	US-10-793-626-1830	Sequence 1830, Ap
36	72.5	5.9	265	7	US-11-087-099-3888	Sequence 3888, Ap
37	72.5	5.9	1228	7	US-11-234-786-537	Sequence 537, App
38	72.5	5.9	1261	7	US-11-234-786-538	Sequence 538, App
39	72.5	5.9	1325	6	US-10-329-258-10	Sequence 10, Appl
40	72.5	5.9	1325	7	US-11-124-367A-410	Sequence 410, Appl
41	72.5	5.9	5712	7	US-11-143-980-47	Sequence 47, Appl
42	72	5.8	263	7	US-11-087-099-9836	Sequence 9836, Ap
43	72	5.8	479	7	US-11-087-099-2356	Sequence 2356, Ap
44	72	5.8	652	7	US-11-079-122-11	Sequence 11, Appl
45	71.5	5.8	112	7	US-11-098-686-11412	Sequence 11412, A

## ALIGNMENTS

### RESULT 1

US-10-506-443A-38  
; Sequence 38, Application US/10506443A  
; Publication No. US20060013817A1  
; GENERAL INFORMATION:  
; APPLICANT: Sahin Dr., Ugur  
; APPLICANT: Tureci Dr., Ozlem  
; APPLICANT: Koslowski Dr., Michael  
; TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use The  
; FILE REFERENCE: 342-3PCT  
; CURRENT APPLICATION NUMBER: US/10/506,443A  
; CURRENT FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-506-443A-38

Query Match 15.0%; Score 186; DB 6; Length 267;

Best Local Similarity 30.5%; Pred. No. 2.9e-11;

Matches 47; Conservative 30; Mismatches 59; Indels 18; Gaps 3;

QY	44	SPPLHTLTLVKKQEFGLQVLTAMICLCFQTVVCSV-LDISHIEGDIFFSFKAGYPF	102
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QY	103	WGAIFFISGMLSIISERRNATYLVRSIGANTASSIAGGTITILINL-----	152
DB	134	WGGLSFIISGSLVSASKLSRCLVKGLGMINIVSILAFIGVILLVDMCINGVAGODY	193
QY	153	-----KSLAYIHHSCKPFETKCFMASPSTE	180
DB	194	WAVLSGKGISATIMIFSLLEFF-VACATAHFANQ	226

### RESULT 2

US-11-138-949-9  
; Sequence 9, Application US/11138949  
; Publication No. US20050271662A1  
; GENERAL INFORMATION:  
; APPLICANT: Beall, Melissa J  
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS  
; FILE REFERENCE: 04-457A  
; CURRENT APPLICATION NUMBER: US/11/138,949  
; CURRENT FILING DATE: 2005-05-26  
; PRIOR APPLICATION NUMBER: 60/575172

; PRIOR FILING DATE: 2004-05-28  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 9  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-11-138-949-9

Query Match 11.9%; Score 147.5; DB 7; Length 298;  
Best Local Similarity 22.6%; Pred. No. 2.5e-07;  
Matches 68; Conservative 48; Mismatches 112; Indels 73; Gaps 12;  
Qy 1 MDTESNRANLALPOEISSVPAFEVLEISPOEVSSGRLLKASPPPLHTWLTVLKKQEF 60  
Db 1 MTTFRNMSG-TLPADAMKST-AMNPVKIPIKMPSVVGTQNFEM---RESKP 51  
Qy 61 LGVTQILTAMICLCFGTVCVSVLDISHIEGDISSFKAGYDFWGAIFFSISGMLSIISER 120  
Db 52 LGAVQIMNGLFHMALGGLL-----MIHVEYVAPICMTVWPLMGIMYIISGSLVAEK 106  
Qy 121 RNATYLRGSLGANTASSIAGGTGTTILIN-----LKKSLAYIHIHS 163  
Db 107 NPKSLVKGKIMNLSLFAAISGMILLIMDIFNIAISHFFKEMENLLKSPKPYIDIHT 166  
Qy 164 CO-----KPFET--KCFMASFSTEIVVMMLFLTILGLG-----SA 196  
Db 167 CQPSKPSKSNLSIKYCDIRSIVLSIFAV-MVVFTLFQKLVTAGIVENEWKLCCKPK 225  
Qy 197 VSLTICGAGBELKGN--KVPEDRV-----YEELNIYSATYSELEDPCGEMS---PPI 242  
Db 226 ADVVLLAAEKKQLVEITEAEVELTEVSSQPKNEEDIEIIPQVEEETEMNFPPEPQ 295  
Qy 243 D 243  
Db 286 D 286

RESULT 3  
US-11-138-949-6  
; Sequence 6, Application US/11138949  
; Publication No. US20050271662A1  
; GENERAL INFORMATION:  
; APPLICANT: Beall, Melissa J  
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS  
; FILE REFERENCE: 04-457A  
; CURRENT APPLICATION NUMBER: US/11/138,949  
; CURRENT FILING DATE: 2005-05-26  
; PRIOR APPLICATION NUMBER: 60/575172  
; PRIOR FILING DATE: 2004-05-28  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 6  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-11-138-949-6

Query Match 11.6%; Score 143.5; DB 7; Length 297;  
Best Local Similarity 24.3%; Pred. No. 6.3e-07;  
Matches 45; Conservative 33; Mismatches 68; Indels 39; Gaps 7;  
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Db 1 MTTFRNMSG-TLPVDPKMSPTAMPYVQKIIPKR-----MPSVVGVTQNFEM---RES 49  
Qy 59 EFLGVTOILTAMICLCFGTVCVSVLDISHIEGDISS--SFKAGYDFWGAIFFSISGMLSI 116  
Db 50 KTLGAVQIMNGLFHIALGSLM-----IHTDYAPICITMWPPLMGIMYIISGSLA 102  
Qy 117 ISERNATYLRGSLGANTASSIAGGTGTTILIN-----LKKSLAYIHIHS 159  
Db 103 AADKNPKSLVKGKIMNLSLFAAISGIIFLIMDIFNITISHFLKXENLNLIKAPIYV 162

Qy 160 HIHSC 164  
Db 163 DIHNC 167

RESULT 4  
US-09-978-360A-610  
; Sequence 610, Application US/09978360A  
; Publication No. US20060009633A9  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56 US4 CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: US 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: US 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
; PRIOR FILING DATE: -09-04  
; PRIOR APPLICATION NUMBER: US 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 09/215,435  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: US 09/247,155  
; PRIOR FILING DATE: 1999-02-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 810  
; SOFTWARE: Patent.pm  
; SEQ ID NO 610  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -69...-1  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (-25, 65, 79, 83, 90, 91, 94, 106, 112, 130, 131, 155)  
; OTHER INFORMATION: unknown  
US-09-978-360A-610

Query Match 10.3%; Score 128; DB 5; Length 248;  
Best Local Similarity 23.2%; Pred. No. 1.8e-05;  
Matches 59; Conservative 35; Mismatches 102; Indels 58; Gaps 9;  
Qy 13 LPQE-----PSSVPAFEVLEISPOEVSSGRLLKASPPPLHTWLTVLKKQEFVGTOIL 67  
Db 6 VNETIIVPSNVINFSQAE-RPEPTNQG-----DSLKKH-----LHAEXKRVIGTQIL 54  
Qy 68 TAMICLCFGTVCVSVL---DISHIEGDISSFKAGYDFWGAIFFSISGMLSIISERNAT 124  
Db 55 CGMWLSLGLIILASASFSNFQVSTLNS---AYFGIPFFFIISGSLIATKRLTN 111  
Qy 125 YLVRSGLANTASSIAGGTGTTILII-----NLKSLAYIHIHSCQKFF 168  
Db 112 LLVHTTLVGSILSALSALVGFXLSVKQATLNPASLXCELXKNINPTXXVXYFYHDSLY 171  
Qy 169 ETKCPMA-SFSTEIVVMMLFLTILGL-----GSAVSLTICGAGBEL 208

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: A\_Geneseq\_21.\*
- 2: Geneseq1980s.\*
- 3: Geneseq1990s.\*
- 4: Geneseq2000s.\*
- 5: Geneseq2001s.\*
- 6: Geneseq2002s.\*
- 7: Geneseq2003as.\*
- 8: Geneseq2003bs.\*
- 9: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1002	100.0	195	4	Aab74448 Human var
2	910	90.8	244	2	Aaw29149 Human hig
3	910	90.8	244	2	Aaw75918 Human bet
4	910	90.8	244	4	Aab72900 Human IGE
5	910	90.8	244	4	Aab74447 Human wil
6	910	90.8	244	5	Abp65043 Human mem
7	910	90.8	244	5	Aau88021 Human IGE
8	910	90.8	244	8	Adq90468 Human IGE
9	492	49.1	235	5	Abp65047 Mouse mem
10	492	49.1	235	5	Aau88020 Mouse IGE
11	492	49.1	235	8	Adq90467 Mouse IGE
12	475	47.4	243	2	Aar42341 Subunit o
13	475	47.4	243	5	Abp65048 Rat membr
14	475	47.4	246	2	Aar14770 Beta subu
15	475	47.4	246	2	Aar42337 Human fce
16	466	46.5	243	2	Aar05026 Beta subu
17	283	28.2	112	2	Aar05027 Deleted f
18	283	28.2	115	2	Aar14771 Truncated
19	189.5	18.9	244	4	Aag63825 Immunogl
20	188.5	18.8	244	5	Abp65036 Mouse mem
21	188.5	18.8	679	5	Adq82232 Human tes
22	187.5	18.7	267	2	Aay15224 Human rec
23	187.5	18.7	267	6	Ada10964 Human CDN
24	187.5	18.7	273	4	Abg17004 Novel hum

25	187.5	18.7	299	3	AAY91352	Human sec
26	187.5	18.7	308	5	ADR41397	Human CD-
27	186.5	18.6	268	5	ABP65040	Mouse mem
28	184	18.4	267	5	ABP65045	Human mem
29	184	18.4	267	7	ADL13125	Human MS4
30	184	18.4	267	9	ADY91718	Human mem
31	184	18.4	267	9	AEA04513	Human pro
32	183	18.3	247	5	ABP65038	Mouse mem
33	182.5	18.2	240	7	ADC42847	REMAP pro
34	182	18.2	247	4	AAE05353	Mouse hig
35	182	18.2	247	5	ABB72363	Murine pr
36	181.5	18.1	307	3	AA91421	Human sec
37	178	17.8	197	7	ADN39134	Cancer/an
38	177	17.7	220	5	ABP65023	Human mem
39	177	17.7	220	6	ABP65023	Human mem
40	177	17.7	220	6	ABP65023	Amino aci
41	177	17.7	220	7	ADN39992	Cancer/an
42	177	17.7	220	8	ADP25105	PKO polyp
43	177	17.7	220	8	ADU06669	Novel bro
44	177	17.7	239	2	Aaw96745	High affi
45	177	17.7	239	3	AAY50174	Human hig

## ALIGNMENTS

RESULT 1  
AAB74448  
ID AAB74448 standard; protein; 195 AA.  
XX  
AC AAB74448;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human variant FcpsiIonRibeta chain.  
XX  
KW Human; FcpsiIonRibeta chain; immunoglobulin E; allergy; atopy;  
KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema.  
XX  
OS Homo sapiens.  
XX  
FN WO200121816-A1.  
XX  
PD 29-MAR-2001.  
XX  
PF 21-SEP-2000; 2000WO-US025877.  
XX  
PR 21-SEP-1999; 99US-0154924P.  
XX  
(ISIS-) ISIS INNOVATION LTD.  
(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;  
XX  
WPI; 2001-266077/27.  
XX  
DR N-PSDB; AAF77689.  
XX  
PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)  
PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IGE, by  
XX contacting cell or administering to subject, a FcERbeta chain variant.  
XX  
PS Claim 5; Page 51; 55pp; English.  
XX  
CC The present invention describes a method of inhibiting the expression of  
CC the FcpsiIonRibeta receptor by contacting a cell expressing it with an  
CC FcpsiIonRibeta chain variant. The FcpsiIonRibeta receptor is a high affinity  
CC receptor for immunoglobulin E. The method is useful in the treatment of  
CC allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis,  
CC urticaria and angioedema. The present sequence is the variant human  
XX FcpsiIonRibeta chain  
XX  
SQ Sequence 195 AA;

Query Match 100.0%; Score 1002; DB 4; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1.7e-105; Indels 0; Gaps 0;  
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKASASPPLHTWLTWLVKKEQEF 60  
DB 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKASASPPLHTWLTWLVKKEQEF 60

QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSFKAGYPPFWGAIFPFSISGMLSIISER 120  
DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSFKAGYPPFWGAIFPFSISGMLSIISER 120

QY 121 RNATYLVRGSLGANTASSIAGGTITILINLKSLAYIHHSCKFFETKCFMASFSTV 180  
DB 121 RNATYLVRGSLGANTASSIAGGTITILINLKSLAYIHHSCKFFETKCFMASFSTV 180

QY 181 CFFCVGRLRFVWLM 195  
DB 181 CFFCVGRLRFVWLM 195

RESULT 2  
AAW29149  
ID AAW29149 standard; protein; 244 AA.  
XX  
AC AAW29149;  
XX  
DT 12-DEC-1997 (first entry)  
XX  
DE Human high affinity IGE receptor beta chain E237G variant.  
XX  
KW human; immunoglobulin E; high affinity receptor; beta subunit; IGE;  
KW Fc epsilon RI beta; exon 7; variant; E237G; atopy; atopic asthma;  
KW detection; diagnosis; polymorphism; subgroup; clinical management.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 237. /note= "E237G variant"  
FT  
XX  
PN WO9708338-A1.  
XX  
PD 06-MAR-1997.  
XX  
PF 29-AUG-1996; 96WO-GB002095.  
XX  
PR 29-AUG-1995; 95GB-00017585.  
XX  
PA (ISIS-) ISIS INNOVATIONS LTD.  
XX  
PI Cookson WOC, Hill MR;  
XX  
DR WPI; 1997-179293/16.  
DR N-PSDB; AAT86756.  
XX  
PT Diagnosing atopy, or predisposition to it - by detection of  
PT immunoglobulin E high affinity receptor beta subunit exon 7 variant  
PT Glu237Gly.  
XX  
PS Disclosure; Page; 25pp; English.  
XX  
CC This is the human immunoglobulin E (IGE) high affinity receptor beta  
CC subunit (Fc epsilon RI beta) exon 7 variant E237G. This variant is  
CC associated with atopy and atopic asthma. The variation is in exon 7 (see  
CC T86756) and is a nucleotide change from adenine to guanine at nucleotide  
CC 7297 (nucleotide 6843 in the Fc epsilon RI beta gene sequence of Kuster,  
CC et al. 1992). Detection of the protein is useful for diagnosis of atopy.  
CC In particular the E237G polymorphism may also define a subgroup of asthma  
CC sufferers with a particular clinical course, in which case recognition of  
CC the variant/polymorphism would be of value in defining asthma prognosis  
CC and management. NB. This sequence was created using the sequence given in  
CC Genbank M89796

XX SQ Sequence 244 AA;  
Query Match 90.8%; Score 910; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 7.3e-95; Indels 0; Gaps 0;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKASASPPLHTWLTWLVKKEQEF 60  
DB 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKASASPPLHTWLTWLVKKEQEF 60

QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSFKAGYPPFWGAIFPFSISGMLSIISER 120  
DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSFKAGYPPFWGAIFPFSISGMLSIISER 120

QY 121 RNATYLVRGSLGANTASSIAGGTITILINLKSLAYIHHSCKFFETKCFMASFST 179  
DB 121 RNATYLVRGSLGANTASSIAGGTITILINLKSLAYIHHSCKFFETKCFMASFST 179

RESULT 3  
AAW75918  
ID AAW75918 standard; protein; 244 AA.  
XX  
AC AAW75918;  
XX  
DT 13-NOV-1998 (first entry)  
XX  
DE Human beta subunit of Fc epsilon RI polypeptide sequence.  
XX  
KW Human beta subunit of Fc epsilon RI; ARAM; Fc epsilon RI beta chain;  
KW antigen recognition activation motif; human beta subunit; allergy;  
KW high-affinity immunoglobulin E receptor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 60..80  
FT /note= "transmembrane domain"  
FT Domain 99..118  
FT /note= "transmembrane domain"  
FT Domain 129..150  
FT /note= "transmembrane domain"  
FT Domain 181..201  
FT /note= "transmembrane domain"  
XX  
PN US5807988-A.  
XX  
PD 15-SEP-1998.  
XX  
PF 24-FEB-1994; 94US-00201879.  
XX  
PR 16-APR-1992; 92US-00869933.  
PR 16-APR-1993; 93WO-US003419.  
XX  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Jouvin M, Kinet J;  
XX  
DR WPI; 1998-520207/44.  
DR N-PSDB; AAV54661.  
XX  
PT Human IGE receptor beta subunit protein - and corresponding peptide(s)  
PT and fusion protein.  
XX  
PS Claim 2; Col 43-44; 55pp; English.  
XX  
CC This represents the polypeptide sequence of a human beta subunit of Fc  
CC epsilon RI [high-affinity immunoglobulin E receptor]. The invention  
CC provides a peptide fragment (AAW75917) from the human Fc epsilon RI beta  
CC subunit protein that contains the amino acid sequence of an ARAM (antigen  
CC recognition activation motif). Aspects of the invention are methods and  
CC compositions to inhibit the function of human beta subunit, thereby

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:45:16 ; Search time 21.7654 Seconds  
(without alignments)  
862.024 Million cell updates/sec

Title: US-10-088-703A-4  
Perfect score: 1002  
Sequence: 1 MDTESNRRANLALPQEPSSV.....SFSTVCIFCVGRLEFWILM 195  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	91.0	90.8	244	A42806	IgE Fc receptor be
2	560	55.9	152	JH0751	IgE receptor beta
3	492	49.1	235	B34342	IgE Fc receptor be
4	475	47.4	243	A31231	high-affinity IgE
5	153	15.3	214	I59258	IgE receptor beta
6	124	12.4	297	A30586	B-cell surface ant
7	113	11.3	200	JC7585	testis expressed t
8	103.5	10.3	291	A30558	B-cell surface ant
9	89	8.9	904	RDNTNT	nitrate reductase
10	85.5	8.5	1235	C69165	hypothetical prote
11	83.5	8.3	466	H81697	amino acid antipor
12	83.5	8.3	669	T08827	hypothetical prote
13	83.5	8.3	4447	A96679	polyketide synthas
14	81.5	8.1	377	G71341	conserved hypothet
15	81	8.1	891	RDHNRP	nitrate reductase
16	80	8.0	904	RDNTNS	nitrate reductase
17	80	8.0	921	E86764	conserved hypothet
18	79.5	7.9	449	G95876	probable permealase
19	79.5	7.9	701	F70155	Na+/H+ antiporter
20	79	7.9	282	S26030	NADH2 dehydrogenas
21	78.5	7.8	659	E86313	hypothetical prote
22	77.5	7.7	362	C88086	protein Tif1.1 (f
23	77	7.7	358	C82281	ferric vibriobacti
24	77	7.7	387	A47287	estradiol 17beta-d
25	77	7.7	917	E96807	nitrate reductase
26	77	7.7	917	S35228	nitrate reductase
27	76.5	7.6	570	S07744	NADH2 dehydrogenas
28	76	7.6	125	D85595	probable membrane
29	76	7.6	125	H90744	probable membrane

30	76	7.6	125	2	H64822	probable membrane
31	76	7.6	229	2	S12593	nonstructural prot
32	76	7.6	463	2	T46290	hypothetical prote
33	76	7.6	764	2	A47456	down-regulated in
34	76	7.6	909	2	JN0665	nitrate reductase
35	76	7.6	1010	2	T33372	hypothetical prote
36	75.5	7.5	596	2	A46414	histidine protein
37	75.5	7.5	597	2	C87381	sensor histidine k
38	75.5	7.5	606	1	QXB05M	NADH2 dehydrogenas
39	75.5	7.5	669	2	S64795	suppressor protein
40	75	7.5	230	1	A42949	CAMP receptor prot
41	75	7.5	258	2	G75372	conserved hypothet
42	75	7.5	449	2	JC5391	presenilin-beta -
43	75	7.5	584	2	D84264	hypothetical prote
44	75	7.5	1053	2	S72194	hydroxymethylgluta
45	75	7.5	4196	2	T43274	dynein heavy chain

ALIGNMENTS

RESULT 1  
A42806  
IgE Fc receptor beta chain - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 09-Jul-2004  
C:Accession: A42806; S21154  
R:Kuester, H.; Zhang, L.; Brini, A.T.; MacGlashan, D.W.J.; Kinet, J.P.  
J. Biol. Chem. 267, 12782-12787, 1992  
A:Title: The gene and cDNA for the human high affinity immunoglobulin E receptor beta  
A:Reference number: A42806; MUID:92316966; PMID:1535625  
A:Accession: A42806  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-244 <KUE>  
A:Cross-references: UNIPROT:Q01362; UNIPARC:UPI0000038B6F; GB:M89796; NID:G337417; PIR  
R:Maekawa, K.; Imagawa, N.; Tanaka, Y.; Harada, S.  
FEBS Lett. 302, 161-165, 1992  
A:Title: Determination of the sequence coding for the beta subunit of the human high-a  
A:Reference number: S21154; MUID:92339505; PMID:1386024  
A:Accession: S21154  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-244 <MAE>  
A:Cross-references: UNIPARC:UPI0000038B6F; GB:D10583; NID:G219881; PIDN:BAA0140.1; PI  
C:Genetics: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3  
A:Introns: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3  
C:Keywords: immunoglobulin receptor; transmembrane protein

Query Match	90.8%;	Score	910;	DB 2;	Length	244;	
Best Local Similarity	100.0%;	Pred. No.	1.4e-80;	Mismatches	0;	Gaps	0;
Matches	179;	Conservative	0;	Indels	0;		
QY	1	MDTESNRRANLALPOEPSSVPAFEVLEISPOQVSSGRLLKSSASSPPLHTLTLVTKKEQEF	60				
Db	1	MDTESNRRANLALPOEPSSVPAFEVLEISPOQVSSGRLLKSSASSPPLHTLTLVTKKEQEF	60				
QY	61	LGVTQILTAMICLCFGTVCSVLDSHIEGDISSFKAGYPFWGAIFFSISGMLSIISER	120				
Db	61	LGVTQILTAMICLCFGTVCSVLDSHIEGDISSFKAGYPFWGAIFFSISGMLSIISER	120				
QY	121	RNATLVVRGSLGANTASSIAGTGITILINLKKSLAYIIHSCQKFFETKCFMASFST	179				
Db	121	RNATLVVRGSLGANTASSIAGTGITILINLKKSLAYIIHSCQKFFETKCFMASFST	179				

RESULT 2  
JH0751  
IgE receptor beta chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: JH0751  
R:Bieber, T.; de la Salle, H.; Wollenberg, A.; Hakiml, J.; Chizzonite, R.; Ring, J.; H



J. Exp. Med. 175, 1285-1290, 1992  
A;Title: Human epidermal Langerhans cells express the high affinity receptor for immunoglobulin E; Keywords: Immunoglobulin receptor; transmembrane protein  
A;Reference number: JH0751; MUID:92235608; PMID:1533242  
A;Accession: JH0751  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-152 <BIE>  
A;Cross-references: UNIPROT:Q14298; UNIPARC:UPI0000073ACE; GB:X66187; NID:9396463; PIDN:  
Query Match 55.9%; Score 560; DB 2; Length 152;  
Best Local Similarity 99.1%; Pred. No. 6.4e-47;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 71 ICLCFGTVCVSLDISHIEGDISSFKAGYFPGWGAIFFSISGMLSIISERNATYLVGRS 130  
DB 1 ICLCFGTVCVSLDISHIEGDISSFKAGYFPGWGAIFFSISGMLSIISERNATYLVGRS 60  
QY 131 LGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETKCPMASFST 179  
DB 61 LGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETKCPMASFST 109  
RESULT 3  
B34342  
IGE Fc receptor beta chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: B34342  
R;Ra, C.; Jouvin, M.H.E.; Kinet, J.P.  
J. Biol. Chem. 264, 15323-15327, 1989  
A;Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) and  
A;Reference number: A34342; MUID:89359361; PMID:2527850  
A;Accession: B34342  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-235 <RAC>  
A;Cross-references: UNIPROT:P20490; UNIPARC:UPI00000223FC; GB:J05019; NID:9193238; PIDN:  
C;Keywords: Immunoglobulin receptor; transmembrane protein  
Query Match 49.1%; Score 492; DB 2; Length 235;  
Best Local Similarity 52.3%; Pred. No. 4.2e-40;  
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;  
QY 1 MDTESNRRANLAL--POEPSVPAFEVLEISPOEVSSGRLLKSSASPPPLHTWTLVKKEQ 58  
DB 1 MDTENSRADLALPNPOESSAPDIELLEASP-----AKAAPPKQTWTFLLKKEQ 50  
QY 59 EFLGVTQILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYFPGWGAIFFSISGMLSIIS 118  
DB 51 EFLGATQILVGLICLCFGTVVCSVLVSDPDEDEVLLYKLGYPFGWGAIFVLSGFLSIIS 110  
QY 119 ERNATYLVRGSLGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETK-CPMASF 177  
DB 111 ERKNTLYLVRGSLGANIVSSIAAGTGIFAMLIILNTNNFAY--MNCKNVETDDGCFVASF 168  
QY 178 STVCIF-----FC 185  
DB 169 TTELVMMLFLTLAFC 185  
RESULT 4  
A31231  
high-affinity IGE receptor beta chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: A31231  
R;Kinet, J.P.; Blank, U.; Ra, C.; White, K.; Metzger, H.; Kochan, J.  
Proc. Natl. Acad. Sci. U.S.A. 85, 6483-6487, 1988  
A;Title: Isolation and characterization of cDNAs coding for the beta-subunit of the high  
A;Reference number: A31231; MUID:88320465; PMID:2970642  
A;Accession: A31231  
A;Molecule type: mRNA  
A;Residues: 1-243 <KIN>

A;Cross-references: UNIPROT:PI3386; UNIPARC:UPI000003FF8D; GB:M22923; GB:J03845; NID:9  
C;Keywords: Immunoglobulin receptor; transmembrane protein  
Query Match 47.4%; Score 475; DB 2; Length 243;  
Best Local Similarity 51.8%; Pred. No. 1.9e-38;  
Matches 102; Conservative 23; Mismatches 56; Indels 16; Gaps 5;  
QY 1 MDTESNRRANLAL--POEPSVPAFEVLEISPOEVSSGRLLKSSASPPPLHTWTLVKKEQ 58  
DB 1 MDTENSRADLALPNPOESSAPDIELLEASPAPKALPE--KPASPPPOQTWQSFLLKKEQ 58  
QY 59 EFLGVTQILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYFPGWGAIFFSISGMLSIIS 118  
DB 59 EFLGVTQILVGLICLCFGTVVCSVLTSQTSDFDDEVLLYKLGYPFGWGAIFVLSGFLSIIS 118  
QY 119 ERNATYLVRGSLGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETK-CPMASF 177  
DB 119 ERKNTLYLVRGSLGANIVSSIAAGLGIAIILNLSNNSAYMNY--CKDITEDDGCFTVSF 176  
QY 178 STVCIF-----FC 185  
DB 177 ITELVMMLFLTLAFC 193  
RESULT 5  
I59258  
IGE receptor beta chain / CD20 antigen homolog - human  
C;Species: Homo sapiens (man)  
C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 05-Nov-1999  
C;Accession: I59258  
R;Adra, C.N.; Laliass, J.M.; Kobayashi, H.; Kaghad, M.; Morrison, P.; Rowley, J.D.; Lin  
Proc. Natl. Acad. Sci. U.S.A. 91, 10178-10182, 1994  
A;Title: Cloning of the cDNA for a hematopoietic cell-specific protein related to CD20  
nning regions.  
A;Reference number: I59258; MUID:95024008; PMID:7524084  
A;Accession: I59258  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-214 <RES>  
A;Cross-references: UNIPARC:UPI000002EF35; GB:L35848; NID:9561638; PIDN:AAA62319.1; PI  
C;Genetics:  
A;Gene: GDB:CD20L; HTM4  
A;Cross-references: GDB:392702  
A;Map position: 11q12-11q13.1  
C;Keywords: Immunoglobulin receptor  
Query Match 15.3%; Score 153; DB 2; Length 214;  
Best Local Similarity 28.8%; Pred. No. 2.6e-07;  
Matches 45; Conservative 26; Mismatches 73; Indels 12; Gaps 5;  
QY 27 EISPOEVSSGRLLKSSASPPPLHTWTLVKKEQFGLVGTQILTAMICLCFGTVVCSVLDS 86  
DB 23 ETGPELNTSVYHPINGSPTYQ-----KAKQLVLGAIQILNAAITLALGVFLGSLOYPY 76  
QY 87 HTEGD-IPSPKAGYFPGWGAIFFSISGMLSIISERNATYLVRGSLGANTASSIAGGTGI 145  
DB 77 HFQKHFFFTFTGTGPIWGAVFCCSGTILSVVAGIKPTFTWTQNSFGMIASATIALVGT 136  
QY 146 TILINLKKSLAYIIHSCQKFFETK--C-FMASFS 178  
DB 137 AFLSLNIQVNIQ--SLRSCHSSSPDLCLNYMGSIS 170  
RESULT 6  
A30586  
B-cell surface antigen CD20 - human  
N;Alternate names: B-lymphocyte antigen CD20; B1  
C;Species: Homo sapiens (man)  
C;Date: 08-Jun-1989 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: A30586; JLO042; A27400; S00387  
R;Tedder, T.F.; Klejman, G.; Schloeman, S.F.; Saito, H.  
J. Immunol. 142, 2560-2568, 1989  
A;Title: Structure of the gene encoding the human B lymphocyte differentiation antigen

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:44:51 ; Search time 143.918 Seconds  
(without alignments)  
955.947 Million cell updates/sec

Title: US-10-088-703A-4  
Perfect score: 1002  
Sequence: 1 MTESNRRNALALPOEPSSV.....SFSTVCIFPCVGRLEFRWLM 195

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	910	90.8	244	1 FCERB_HUMAN	Q01362 homo sapien
2	910	90.8	244	2 Q5A81_HUMAN	Q5A81 homo sapien
3	560	55.9	152	2 Q14298_HUMAN	Q14298 homo sapien
4	492	49.1	235	1 FCERB_MOUSE	P20490 mus musculus
5	481.5	48.1	243	2 Q8WJ38_PIG	Q8WJ38 sus scrofa
6	475	47.4	243	1 FCERB_RAT	P13386 rattus norv
7	188.5	18.8	244	1 M4A6B_MOUSE	Q95N09 mus musculus
8	188.5	18.8	247	2 Q5XJ70_RAT	Q5XJ70 rattus norv
9	188.5	18.8	679	2 Q96J44_HUMAN	Q96J44 homo sapien
10	187.5	18.7	267	1 M4A12_HUMAN	Q9N10 homo sapien
11	186.5	18.6	287	1 M4A8A_MOUSE	Q99N07 mus musculus
12	183	18.3	247	1 M4A6D_MOUSE	Q96J45 homo sapien
13	177	17.7	239	1 M4A4A_HUMAN	Q96J19 homo sapien
14	174.5	17.4	250	1 M4A8B_HUMAN	Q96J19 homo sapien
15	171	17.1	220	2 Q4JF27_HUMAN	Q4JF27 homo sapien
16	156.5	15.6	217	1 M4A6C_MOUSE	Q99N08 mus musculus
17	154.5	15.4	241	2 Q567K1_BRARE	Q567K1 brachydanio
18	154	15.4	214	1 M5A43_HUMAN	Q96J45 homo sapien
19	153	15.3	222	2 Q58DM5_BOVIN	Q58DM5 bos taurus
20	149.5	14.9	213	1 M5A43_MOUSE	Q920C4 mus musculus
21	149.5	14.9	213	2 Q810H7_MOUSE	Q810H7 mus musculus
22	149.5	14.9	213	2 Q53ZU3_MOUSE	Q53ZU3 mus musculus
23	149	14.9	205	2 Q8BL29_MOUSE	Q8BL29 mus musculus
24	149	14.9	234	2 Q99N04_MOUSE	Q99N04 mus musculus
25	146	14.6	267	2 Q8BV59_MOUSE	Q8BV59 mus musculus
26	145	14.5	234	2 Q83W1_MOUSE	Q83W1 mus musculus
27	144.5	14.4	197	2 Q810P8_MOUSE	Q810P8 mus musculus
28	143.5	14.3	240	1 M5A47_HUMAN	Q9GZW8 homo sapien
29	143.5	14.3	240	2 Q6TAG8_HUMAN	Q6TAG8 homo sapien
30	142	14.2	298	2 Q5R1M8_FELCA	Q5R1M8 felis silve
31	138	13.8	248	1 M4A6A_HUMAN	Q9H2W1 homo sapien

32	135.5	13.5	252	2 Q567H8_BRARE	Q567H8 brachydanio
33	129.5	12.9	234	2 Q66ID5_BRARE	Q66ID5 brachydanio
34	129.5	12.9	1139	2 Q80WF0_RAT	Q80WF0 rattus norv
35	126.5	12.6	226	2 Q9D3F6_MOUSE	Q9D3F6 mus musculus
36	126	12.6	147	2 Q8NSU1_HUMAN	Q8NSU1 homo sapien
37	124	12.4	297	1 CD20_HUMAN	P11936 homo sapien
38	120	12.0	241	2 Q5BLB6_BRARE	Q5BLB6 brachydanio
39	120	12.0	267	1 M4A10_HUMAN	Q96PG2 homo sapien
40	118.5	11.8	183	2 Q8C2D9_MOUSE	Q8C2D9 mus musculus
41	118.5	11.8	226	2 Q9S61_MOUSE	Q9S61 mus musculus
42	116	11.6	264	2 Q5REZ5_PONPY	Q5REZ5 pongo pygma
43	115	11.5	231	2 Q5M796_XENTR	Q5M796 xenopus tro
44	113.5	11.3	135	2 Q95LT4_MACFA	Q95LT4 macaca fasc
45	113.5	11.3	170	2 Q4R3P9_MACFA	Q4R3P9 macaca fasc

## ALIGNMENTS

RESULT 1  
FCERB\_HUMAN  
ID FCERB\_HUMAN STANDARD; PRT; 244 AA.  
AC Q01362;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DE High affinity immunoglobulin epsilon receptor beta-subunit (FcERI)  
DE (Ige Fc receptor, beta-subunit) (Fc epsilon receptor I beta-chain).  
GN Name=MS4A2; Synonyms=FCER1B, IGER;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92316966; PubMed=1535625;  
RA Kuester H., Zhang L., Brini A.T., Macglashan D.W., Kinet J.-P.;  
RT "The gene and cDNA for the human high affinity immunoglobulin E  
receptor beta chain and expression of the complete human receptor.";  
RL J. Biol. Chem. 267:12782-12787(1992).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=1386024; DOI=10.1016/0014-5793(92)80430-O;  
RA Maekawa K., Imagawa N., Tanaka Y., Harada S.;  
RT "Determination of the sequence coding for the beta subunit of the  
human high-affinity IGE receptor.";  
RL FEBS Lett. 302:161-165(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Richardson S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield V.S.N., Kravinsky M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]

RP VARIANT GLY-237.  
RX MEDLINE=96414302; PubMed=8817330; DOI=10.1093/hmg/5.7.959;  
RA Hill M.R., Cookson W.O.;  
RT "A new variant of the beta subunit of the high-affinity receptor for  
RT immunoglobulin E (Fc epsilon RI-beta E237G): associations with  
RT measures of atopy and bronchial hyper-responsiveness.";  
RL Hum. Mol. Genet. 5:959-962(1996).  
RN [5]  
RP VARIANT GLY-237.  
RX MEDLINE=96440420; PubMed=8842731; DOI=10.1093/hmg/5.8.1129;  
RA Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,  
RA Hopkin J.;  
RT "Association between atopic asthma and a coding variant of Fc-epsilon-  
RT RI-beta in a Japanese population.";  
RL Hum. Mol. Genet. 5:1129-1130(1996).  
RN [6]  
RP ERRATUM.  
RX MEDLINE=97123518; PubMed=8968765;  
RA Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,  
RA Hopkin J.;  
RL Hum. Mol. Genet. 5:2068-2068(1996).  
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins epsilon. High  
CC affinity receptor. Responsible for initiating the allergic  
CC response. Binding of allergen to receptor-bound IgE leads to cell  
CC activation and the release of mediators (such as histamine)  
CC responsible for the manifestations of allergy. The same receptor  
CC also induces the secretion of important lymphokines.  
CC -!- SUBUNIT: Tetramer of an alpha chain, a beta chain, and two  
CC disulfide linked gamma chains.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Found on the surface of mast cells and  
CC basophils.  
CC -!- POLYMORPHISM: Variant Glu-237 has been found to be present in  
CC about 5.3% of a 1004 individuals population sample in Australia.  
CC It seems to be a risk factor for atopic dermatitis and asthma.  
CC -!- SIMILARITY: Belongs to the MS4A family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; D10583; BAA01440.1; -; mRNA.  
CC EMBL; M89796; AAA60269.1; -; Genomic DNA.  
CC EMBL; BC074800; AAH74800.1; -; mRNA.  
CC EMBL; BC074803; AAH74843.1; -; mRNA.  
CC PIR; A42806; A42806.  
CC Ensembl; ENSG00000149534; Homo sapiens.  
CC HGNC; HGNC:7316; MS4A2.  
CC MIM; 147138; -.  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0005262; F:calcium channel activity; TAS.  
CC GO; GO:0008283; P:cell proliferation; TAS.  
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.  
CC GO; GO:0006959; P:humoral immune response; TAS.  
CC InterPro; IPR007237; CD20/IgEfcrcrcept.  
CC Pfam; PF04103; CD20; 1.  
CC IgE-binding protein; Multigene family; Polymorphism; Receptor;  
CC Transmembrane.  
KW TOPO\_DOM 1 59 Cytoplasmic (Potential).  
KW TRANSMEM 60 79 Potential.  
KW TOPO\_DOM 80 97 Extracellular (Potential).  
KW TRANSMEM 98 117 Potential.  
KW TOPO\_DOM 118 130 Cytoplasmic (Potential).  
KW TRANSMEM 131 150 Potential.  
KW TOPO\_DOM 151 180 Extracellular (Potential).  
KW TRANSMEM 181 200 Potential.  
KW TOPO\_DOM 201 244 Cytoplasmic (Potential).  
KW VARIANT 237 237 E -> G (in dbSNP:569108).  
KW SEQUENCE 244 AA; 26534 MW; CE523102D5F567AF CRC64;

Query Match 90.8%; Score 910; DB 1; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2e-80;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDTESNRANLALPOEPSVPAFAVELEISPOEVSSGRLLKKSASSPPLHTLTLVTKKEQEF 60  
DB 1 MDTESNRANLALPOEPSVPAFAVELEISPOEVSSGRLLKKSASSPPLHTLTLVTKKEQEF 60  
QY 61 LGVTOILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYPFWGAIFFSISGMLSIISER 120  
DB 61 LGVTOILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYPFWGAIFFSISGMLSIISER 120  
QY 121 RNATYLVGRSGANTASSIAGGTGTTILINLKSLAYIHHSCKPFETKCFMASFST 179  
DB 121 RNATYLVGRSGANTASSIAGGTGTTILINLKSLAYIHHSCKPFETKCFMASFST 179  
RESULT 2  
Q54A81 HUMAN PRELIMINARY; PRT; 244 AA.  
ID Q54A81 HUMAN PRELIMINARY; PRT; 244 AA.  
AC Q54A81;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Fc-epsilon receptor I beta-chain.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=12697656; DOI=10.1093/intimm/dxg055;  
RA Akizawa Y., Nishiyama C., Hasegawa M., Maeda K., Nakahata T.,  
RA Okumura K., Ra C., Ogawa H.;  
RT "Regulation of human FcepsilonRI beta chain gene expression by Oct-  
RT 1.";  
RL Int. Immunol. 15:549-556(2003).  
KW EMBL; AB080913; BAC66486.1; -; Genomic DNA.  
KW Receptor.  
SQ SEQUENCE 244 AA; 26533 MW; CE523102D5F567AF CRC64;  
Query Match 90.8%; Score 910; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2e-80;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDTESNRANLALPOEPSVPAFAVELEISPOEVSSGRLLKKSASSPPLHTLTLVTKKEQEF 60  
DB 1 MDTESNRANLALPOEPSVPAFAVELEISPOEVSSGRLLKKSASSPPLHTLTLVTKKEQEF 60  
QY 61 LGVTOILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYPFWGAIFFSISGMLSIISER 120  
DB 61 LGVTOILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYPFWGAIFFSISGMLSIISER 120  
QY 121 RNATYLVGRSGANTASSIAGGTGTTILINLKSLAYIHHSCKPFETKCFMASFST 179  
DB 121 RNATYLVGRSGANTASSIAGGTGTTILINLKSLAYIHHSCKPFETKCFMASFST 179  
RESULT 3  
Q14298 HUMAN PRELIMINARY; PRT; 152 AA.  
ID Q14298 HUMAN PRELIMINARY; PRT; 152 AA.  
AC Q14298;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Fc epsilon protein (Fragment).  
GN Name=Fc epsilon;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OC NCBI\_TaxID=9606;

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 18:46:52 ; Search time 16.4351 seconds  
(without alignments)  
980.936 Million cell updates/sec

Title: US-10-088-703a-4  
Perfect score: 1002  
Sequence: 1 MDTESNRRANLALPOEPSSV.....SPTVCIFPCVGRRLRFWLM 195

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PCUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	910	90.8	244	1 US-07-869-933-32	Sequence 32, Appl
2	910	90.8	244	1 US-08-201-879A-3	Sequence 3, Appl
3	910	90.8	244	2 US-09-103-663-32	Sequence 32, Appl
4	910	90.8	244	2 US-09-949-016-5892	Sequence 5892, Ap
5	910	90.8	256	2 US-09-949-016-8329	Sequence 8329, Ap
6	492	49.1	235	1 US-07-869-933-34	Sequence 34, Appl
7	492	49.1	235	1 US-08-201-879A-5	Sequence 5, Appl
8	492	49.1	235	2 US-09-103-663-34	Sequence 34, Appl
9	475	47.4	243	1 US-07-869-933-29	Sequence 29, Appl
10	475	47.4	243	1 US-07-869-933-33	Sequence 33, Appl
11	475	47.4	243	1 US-08-201-879A-4	Sequence 4, Appl
12	475	47.4	243	1 US-08-916-902A-4	Sequence 4, Appl
13	475	47.4	243	1 US-09-213-389-4	Sequence 4, Appl
14	475	47.4	243	2 US-09-103-663-29	Sequence 29, Appl
15	475	47.4	243	2 US-09-103-663-33	Sequence 33, Appl
16	475	47.4	246	1 US-07-869-933-23	Sequence 23, Appl
17	475	47.4	246	1 US-09-103-663-23	Sequence 23, Appl
18	187.5	18.7	239	2 US-09-904-615-73	Sequence 73, Appl
19	187.5	18.7	239	2 US-10-054-988-73	Sequence 73, Appl
20	182	18.2	247	2 US-09-724-864-49	Sequence 49, Appl
21	181.5	18.1	307	2 US-09-904-615-142	Sequence 142, App
22	181.5	18.1	307	2 US-10-054-988-142	Sequence 142, App
23	177	17.7	239	1 US-08-916-902A-1	Sequence 1, Appl
24	177	17.7	239	1 US-09-213-389-1	Sequence 1, Appl
25	177	17.7	239	2 US-10-164-595-74	Sequence 74, Appl
26	174.5	17.4	250	2 US-09-702-705-1677	Sequence 1677, Ap
27	174.5	17.4	250	2 US-09-736-457-1677	Sequence 1677, Ap

28	174.5	17.4	250	2 US-09-671-325-1677	Sequence 1677, Ap
29	174.5	17.4	250	2 US-09-658-824-1677	Sequence 1677, Ap
30	174.5	17.4	250	2 US-10-017-754-1677	Sequence 1677, Ap
31	174.5	17.4	250	2 US-10-017-754-2004	Sequence 2004, Ap
32	174.5	17.4	250	2 US-09-651-563-1677	Sequence 1677, Ap
33	166.5	16.6	250	2 US-10-017-754-1874	Sequence 1874, Ap
34	166.5	16.6	286	2 US-10-017-754-1876	Sequence 1876, Ap
35	166.5	16.6	384	2 US-10-017-754-1876	Sequence 1876, Ap
36	153	15.3	214	1 US-08-318-492-4	Sequence 4, Appl
37	153	15.3	214	1 US-08-707-340-4	Sequence 4, Appl
38	153	15.3	214	1 US-08-916-902A-3	Sequence 3, Appl
39	153	15.3	214	1 US-08-994-578-4	Sequence 4, Appl
40	153	15.3	214	1 US-09-213-389-3	Sequence 3, Appl
41	142	14.2	204	2 US-09-904-615-117	Sequence 117, App
42	142	14.2	204	2 US-10-054-988-117	Sequence 117, App
43	138	13.8	225	2 US-09-855-323-14	Sequence 14, Appl
44	138	13.8	242	2 US-09-311-021-212	Sequence 212, App
45	138	13.8	248	2 US-09-489-847-207	Sequence 207, App

## ALIGNMENTS

RESULT 1  
US-07-869-933-32  
; Sequence 32, Application US/07869933  
; Patent No. 5770396  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/869,933  
; FILING DATE: 19920416  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; STRAIN: FcR1 beta subunit  
; US-07-869-933-32

Query Match 90.8%; Score 910; DB 1; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2e-102;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRRANLALPOEPSSVPAFEVLEISQEVSSGRLLKSSAPPLHTWLTVLKKEQEF 60

Db 1 MDTESNRANLALPOEPSSVPAFEVLEISQEVSSGRLLKSSAPPLHTLTLVLKKEQF 60  
QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
Db 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
QY 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179  
Db 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179

## RESULT 2

US-08-201-879A-3  
; Sequence 3, Application US/08201879A  
; Patent No. 5807988  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; APPLICANT: JOUVIN, Marie-Helene  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; TITLE OF INVENTION: IMMUNOGLOBULIN E  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/201,879A  
; FILING DATE: 24-FEB-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/869,933  
; FILING DATE: 16-APR-1992  
; PRIOR APPLICATION DATA: PCT/US93/03419  
; FILING DATE: 16-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 40399/234/NIHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-201-879A-3

Query Match 90.8%; Score 910; DB 1; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2e-102;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDTESNRANLALPOEPSSVPAFEVLEISQEVSSGRLLKSSAPPLHTLTLVLKKEQF 60  
Db 1 MDTESNRANLALPOEPSSVPAFEVLEISQEVSSGRLLKSSAPPLHTLTLVLKKEQF 60  
QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
Db 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120

QY 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179  
Db 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179

## RESULT 3

US-09-103-663-32  
; Sequence 32, Application US/09103663D  
; Patent No. 6171803  
; GENERAL INFORMATION:  
; APPLICANT: Kinet et al.  
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta  
; TITLE OF INVENTION: subunit of the high affinity receptor for  
; TITLE OF INVENTION: immunoglobulin E.  
; FILE REFERENCE: 50490  
; CURRENT APPLICATION NUMBER: US/09/103,663D  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 07/869,933  
; EARLIER FILING DATE: 1992-04-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent-in-ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-103-663-32

Query Match 90.8%; Score 910; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2e-102;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISQEVSSGRLLKSSAPPLHTLTLVLKKEQF 60  
Db 1 MDTESNRANLALPOEPSSVPAFEVLEISQEVSSGRLLKSSAPPLHTLTLVLKKEQF 60  
QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
Db 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120  
QY 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179  
Db 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179

## RESULT 4

US-09-949-016-5892  
; Sequence 5892, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows version 4.0  
; SEQ ID NO 5892  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5892

Query Match 90.8%; Score 910; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2e-102;  
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:50:58 ; Search-time 54.1913 Seconds  
(without alignments)  
1503.501 Million cell updates/sec

Title: US-10-088-703A-4  
Perfect score: 1002  
Sequence: 1 MDTESNRRANLALPQBSPV.....SFSTVCIFPCVGRRLRFWVLM 195

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	910	90.8	244	4	US-10-369-214-124
2	910	90.8	244	4	US-10-433-287-42
3	492	49.1	235	4	US-10-369-214-123
4	492	49.1	235	4	US-10-433-287-50
5	475	47.4	243	4	US-10-433-287-52
6	188.5	18.8	244	4	US-10-433-287-28
7	187.5	18.7	267	3	US-09-981-253-82
8	187.5	18.7	273	5	US-10-450-763-47363
9	187.5	18.7	299	3	US-09-739-254-73
10	187.5	18.7	299	3	US-09-504-615-73
11	187.5	18.7	299	4	US-10-054-988-73
12	186.5	18.6	268	4	US-10-433-287-36
13	184	18.4	267	4	US-10-433-287-46
14	183	18.3	247	4	US-10-433-287-32
15	182.5	18.2	240	5	US-10-484-148-7
16	182	18.2	247	3	US-09-866-050A-687
17	181.5	18.1	307	3	US-09-739-254-142
18	181.5	18.1	307	3	US-09-904-615-142
19	181.5	18.1	307	4	US-10-054-988-142
20	178	17.8	197	4	US-10-295-027-452
21	177	17.7	220	4	US-10-015-115-103
22	177	17.7	220	4	US-10-295-027-1310
23	177	17.7	220	4	US-10-264-237-2693
24	177	17.7	220	4	US-10-433-287-2
25	177	17.7	239	4	US-10-015-115-101
26	177	17.7	239	4	US-10-015-115-102
27	177	17.7	239	5	US-10-717-665-74

28	177	17.7	245	3	US-09-374-046A-152	Sequence 152, App
29	177	17.7	245	3	US-10-616-263-152	Sequence 152, App
30	174.5	17.4	250	3	US-09-736-457-1677	Sequence 1677, App
31	174.5	17.4	250	3	US-09-902-941-1677	Sequence 1677, App
32	174.5	17.4	250	3	US-09-849-626-1677	Sequence 1677, App
33	174.5	17.4	250	4	US-10-017-754-1677	Sequence 1677, App
34	174.5	17.4	250	4	US-10-017-754-2004	Sequence 2004, App
35	174.5	17.4	250	4	US-10-156-136-21	Sequence 21, Appl
36	174.5	17.4	250	4	US-10-113-872-1677	Sequence 1677, App
37	174.5	17.4	250	4	US-10-113-872-2004	Sequence 2004, App
38	174.5	17.4	250	4	US-10-283-017-1677	Sequence 1677, App
39	174.5	17.4	250	4	US-10-283-017-2004	Sequence 2004, App
40	174.5	17.4	250	4	US-10-295-027-624	Sequence 624, App
41	174.5	17.4	250	4	US-10-264-237-2566	Sequence 2566, App
42	174.5	17.4	250	4	US-10-433-287-16	Sequence 16, Appl
43	174.5	17.4	250	6	US-11-041-419-21	Sequence 21, Appl
44	174.5	17.4	302	3	US-09-925-297-764	Sequence 764, App
45	169.5	16.9	227	5	US-10-450-763-49595	Sequence 49595, A

## ALIGNMENTS

### RESULT 1

US-10-369-214-124  
; Sequence 124, Application US/10369214  
; Publication No. US20030232037A1  
; GENERAL INFORMATION:  
; APPLICANT: Groot, Pieter C.  
; APPLICANT: Berghenhegouwen van, Bram J.  
; APPLICANT: Oosterhout van, Antoon J.M.  
; TITLE OF INVENTION: Genes involved in immune related responses observed  
; TITLE OF INVENTION: with asthma  
; FILE REFERENCE: P53837US00  
; CURRENT APPLICATION NUMBER: US/10/369,214  
; CURRENT FILING DATE: 2003-02-15  
; PRIOR APPLICATION NUMBER: EP 00202867.8  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: PCT/NL01/00610  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 124  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(244)  
; OTHER INFORMATION: /note="Ige receptor beta chain"  
US-10-369-214-124

Query Match	90.8%	Score	910	DB	4	Length	244
Best Local Similarity	100.0%	Pred. No.	6.3e+90	Mismatches	0	Indels	0
Matches	179	Conservative	0	Indels	0	Gaps	0
QY	1	MDTESNRRANLALPQBSPVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF	60				
Db	1	MDTESNRRANLALPQBSPVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF	60				
QY	61	LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYFPWGAIFFSISGMLSIISER	120				
Db	61	LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYFPWGAIFFSISGMLSIISER	120				
QY	121	RNATYLVRSGLGANTASSIAGTGTTILINLKSLAYTHIHSCQKFFETKCFMASFST	179				
Db	121	RNATYLVRSGLGANTASSIAGTGTTILINLKSLAYTHIHSCQKFFETKCFMASFST	179				

### RESULT 2

US-10-433-287-42  
; Sequence 42, Application US/10433287  
; Publication No. US20040137566A1

```
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-433-287-42

Query Match      90.8%; Score 910; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 6.3e-90;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSVPFAFEVLEISPOEVSSGRLLKSASSPPLHTLTLVKKEQEF 60
DB 1 MDTESNRANLALPOEPSVPFAFEVLEISPOEVSSGRLLKSASSPPLHTLTLVKKEQEF 60
QY 61 LGVTOILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
DB 61 LGVTOILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETKCFMASFST 179
DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETKCFMASFST 179

RESULT 3
US-10-369-214-123
; Sequence 123, Application US/10369214
; Publication No. US20030232037A1
; GENERAL INFORMATION:
; APPLICANT: Groot, Pieter C.
; APPLICANT: Berghenhegouwen van, Bram J.
; APPLICANT: Oosterhout van, Antoon J.M.
; TITLE OF INVENTION: Genes involved in immune related responses observed
; TITLE OF INVENTION: with asthma
; FILE REFERENCE: P53837US00
; CURRENT APPLICATION NUMBER: US/10/369,214
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: EP 00202867.8
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00610
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 123
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(235)
; OTHER INFORMATION: /note="Ige receptor beta chain"
; US-10-369-214-123

Query Match      49.1%; Score 492; DB 4; Length 235;
Best Local Similarity 52.3%; Pred. No. 1.3e-44;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;

QY 1 MDTESNRANLAL--POEPSVPFAFEVLEISPOEVSSGRLLKSASSPPLHTLTLVKKEQ 58
DB 1 MDTESNRADLALPNQESSAPDIELLEASP-----AKAAPKQTWRTFLKXEL 50
QY 59 EFLGVTQILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIIS 118
DB 51 EFLGATQILVGLICLCFGTVVCSVLYVSDPEDEVLLLYKLGYPFWGAVLVLSGFLSIIS 110
QY 119 ERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETK-CFMASF 177
DB 111 ERKNTYLVRSGLGANIVSSIAAGTGIAMLINLTNNFAY--MNNCKNVTEDDCCFVASF 168

Query Match      47.4%; Score 475; DB 4; Length 243;
Best Local Similarity 51.8%; Pred. No. 9.4e-43;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;
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QY 119 ERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETK-CFMASF 177
DB 111 ERKNTYLVRSGLGANIVSSIAAGTGIAMLINLTNNFAY--MNNCKNVTEDDCCFVASF 168
QY 178 STVCIF-----FC 185
DB 169 TTELVLMLFLTLAFC 185

RESULT 4
US-10-433-287-50
; Sequence 50, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 50
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-433-287-50

Query Match      49.1%; Score 492; DB 4; Length 235;
Best Local Similarity 52.3%; Pred. No. 1.3e-44;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;

QY 1 MDTESNRANLAL--POEPSVPFAFEVLEISPOEVSSGRLLKSASSPPLHTLTLVKKEQ 58
DB 1 MDTESNRADLALPNQESSAPDIELLEASP-----AKAAPKQTWRTFLKXEL 50
QY 59 EFLGVTQILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIIS 118
DB 51 EFLGATQILVGLICLCFGTVVCSVLYVSDPEDEVLLLYKLGYPFWGAVLVLSGFLSIIS 110
QY 119 ERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETK-CFMASF 177
DB 111 ERKNTYLVRSGLGANIVSSIAAGTGIAMLINLTNNFAY--MNNCKNVTEDDCCFVASF 168
QY 178 STVCIF-----FC 185
DB 169 TTELVLMLFLTLAFC 185

RESULT 5
US-10-433-287-52
; Sequence 52, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 52
; LENGTH: 243
; TYPE: PRT
; ORGANISM: rat
; US-10-433-287-52

Query Match      47.4%; Score 475; DB 4; Length 243;
Best Local Similarity 51.8%; Pred. No. 9.4e-43;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;
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Result No.	Score	Match	Length	ID	Description
1	184	18.4	267	6	US-10-506-443A-38
2	143.5	14.3	297	7	US-11-138-949-6
3	142	14.2	298	7	US-11-138-949-9
4	124.5	12.4	297	7	US-11-190-364-25
5	124.5	12.4	297	7	US-11-147-780-25
6	124	12.4	297	7	US-11-138-949-7
7	124	12.4	297	7	US-11-190-364-26
8	124	12.4	297	7	US-11-147-780-26
9	118	11.8	248	5	US-09-978-360A-610
10	113	11.3	199	7	US-11-179-018-2
11	103.5	10.3	291	7	US-11-138-949-8
12	100	10.0	138	7	US-11-179-018-6
13	99.5	9.9	149	7	US-11-179-018-9
14	83.5	8.3	230	7	US-11-075-512-3554
15	77	7.7	394	6	US-10-821-234-1194
16	75	7.5	509	7	US-11-098-686-10325
17	74	7.4	172	7	US-11-036-797-36
18	72.5	7.2	5712	7	US-11-143-980-47
19	71.5	7.1	345	7	US-11-174-816-44
20	71.5	7.1	345	7	US-11-174-819-13
21	71.5	7.1	473	7	US-11-098-686-10759
22	71	7.1	538	7	US-11-113-683-1
23	71	7.1	801	6	US-10-453-372-468
24	70.5	7.0	7968	7	US-11-143-980-49
25	70	7.0	162	6	US-10-467-657-5624
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					Sequence 6, Appl
					Sequence 9, Appl
					Sequence 25, Appl
					Sequence 25, Appl
					Sequence 7, Appl
					Sequence 26, Appl
					Sequence 26, Appl
					Sequence 610, App
					Sequence 2, Appl
					Sequence 8, Appl
					Sequence 8, Appl
					Sequence 3554, Ap
					Sequence 1194, Ap
					Sequence 10325, A
					Sequence 36, Appl
					Sequence 47, Appl
					Sequence 44, Appl
					Sequence 13, Appl
					Sequence 10759, A
					Sequence 1, Appl
					Sequence 468, App
					Sequence 49, Appl
					Sequence 5624, Ap

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; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-138-949-6

Query Match      14.3%; Score 143.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 8.7e-08;
Matches 45; Conservative 33; Mismatches 68; Indels 39; Gaps 7;

QY 1 MDTESRRNALPQEPSSVPA--FEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQF 58
Db 1 MTTPRNSMSG-TLPVDPMKSPATAMPVQKIIPK-----MPSVVGPTQNFPM-----RES 49
QY 59 EFLGVTOILTAMICLCFGTVVCSVLDSHIEGDIFS--SFKAGYPPFWGAIFFSISGMLSI 116
Db 50 KTLGAVQIMNGLFHIALGSLM-----IHTDVIAPICITWVYPLWGGIMFIISGSLLA 102
QY 117 ISERNATYLRVSGLGANTASSIAGGTGITILIN-----LKKSLAYI 159
Db 103 AADKNPKSLVKGKRWNNLSLFAAISGIIFLIMDIFNIITISHFLKMNENLNLIKAPIYV 162
QY 160 HIHSC 164
Db 163 DIHNC 167

RESULT 3
US-11-138-949-9
; Sequence 9, Application US/11138949
; Publication No. US20050271662A1
; GENERAL INFORMATION:
; APPLICANT: Beall, Melissa J
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS
; FILE REFERENCE: 04-457A
; CURRENT APPLICATION NUMBER: US/11/138,949
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575172
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Felis catus
US-11-138-949-9

Query Match      14.2%; Score 142; DB 7; Length 298;
Best Local Similarity 22.8%; Pred. No. 1.3e-07;
Matches 49; Conservative 39; Mismatches 81; Indels 46; Gaps 7;

QY 1 MDTESRRNALPQEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQF 60
Db 1 MTTPRNSMSG-TLPADAMKSP-----AMNPVQKIIPKMPSVVGPTQNFPM-----KESKP 51
QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDIFSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 52 LGAVQIMNGLFHIALGSL-----MIMNEVYAPICITWVYPLWGGIMFIISGSLVAEK 106
QY 121 RNATYLRVSGLGANTASSIAGGTGITILIN-----LKKSLAYIHIHS 163
Db 107 NPKSLVKGKRWNNLSLFAAISGMILLIMDIFNIALSHFFKNENLNLLKSPKPYDIHT 166
QY 164 CO-----KPFET--KCFMASFSTVCIF 183
Db 167 CQESKPKSEKNSLSIKYCDIRSIVFLSIFAMVVF 201

RESULT 4
US-11-190-364-25

; Sequence 25, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 25
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-190-364-25

Query Match      12.4%; Score 124.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 9.3e-06;
Matches 42; Conservative 30; Mismatches 74; Indels 27; Gaps 6;

QY 3 TESNRRNALPQEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQF 62
Db 2 TTPRNSVNGTTPAEPKMGK-----IAMQPGKPLLRMSLVGPTQSFPM-----RESKALG 53
QY 63 VTQILTAMICLCFGTVVCSVLDSHIEGDIFS--KAGYPPFWGAIFFSISGMLSIISER 120
Db 54 AVQIMNGLFHIALGGLM-----IPAGIYAPICITWVYPLWGGIMFIISGSLAATEK 106
QY 121 RNATYLRVSGLGANTASSIAGGTGITIL-----INLK-----KSLAYIHIHS 163
Db 107 NSRKCLVKGKRWNNLSLFAAISGMILSIMDILNIKISHFLKMNENLNIRVHT 159

RESULT 5
US-11-147-780-25
; Sequence 25, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 25
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-147-780-25

Query Match      12.4%; Score 124.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 9.3e-06;
Matches 42; Conservative 30; Mismatches 74; Indels 27; Gaps 6;

QY 3 TESNRRNALPQEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQF 62
Db 2 TTPRNSVNGTTPAEPKMGK-----IAMQPGKPLLRMSLVGPTQSFPM-----RESKALG 53
QY 63 VTQILTAMICLCFGTVVCSVLDSHIEGDIFS--KAGYPPFWGAIFFSISGMLSIISER 120
Db 54 AVQIMNGLFHIALGGLM-----IPAGIYAPICITWVYPLWGGIMFIISGSLAATEK 106
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